

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 141260

TO: Anish Gupta

Location: REM-3C15&3C18

Art Unit: 1654

Wednesday, December 29, 2004

Case Serial Number: 09/823418

From: Edward Hart

**Location: Biotech-Chem Library** 

**REM-1A55** 

Phone: 571-272-2512

edward.hart@uspto.gov

#### Search Notes

Examiner Gupta,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions

.rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .



This Page Blank (uspto)

#### STiC-Biotech/ChemLib

41260

From:

Gupta, Anish

Sent:

Monday, December 27, 2004 2:39 PM

To: Subject: STIC-Biotech/ChemLib RE: search request

Serial Number: 09 / 823418

Art Unit: 1654

Room:

Remsen 3C15 Mailbox Room: Remsen 3C18

Please search sequence ID No. 2, 3, 4, 5, 6, 7, 8, 13 and 14

Anish Gupta 2-0859 Remsen.

#### Protein Sequence Searches - 10/8/04

All of the sequence databases on the ABSS have been updated. A change has occurred in the protein databases.

- Two protein databases, SPTREMBL and SwissProt, are now produced as a single, merged database called UniProt.
- Results from UniProt have the file extension .rup.
- Sequences in UniProt are identified by the same ID that had been used in SPTREMBL or SwissProt.
- In instances where the database curators have determined that an SPTREMBL record and a SwissProt record represent the same sequence, the two records have been merged into one. Both: IDs are present in the record. Any differences found between the two sequences are recorded in the FT (feature table) fields.

If you have any questions regarding these changes or your results, please contact any STIC searcher.

STAFF USE ONLY	
Searcher:	. ,
Searcher Phone: 2-	. halau
Searcher Phone: 2- Date Searcher Picked up:	M2007
Date Completed: / X	129/anci
Searcher Prep/Rev. Time:	12 11 P (
Online Time:	

\*\*\*\*\*\*\*

Type of Search	
NA Sequence: #	
AA Sequence :#	4
Structure: #	
Bibliographic:	
Litigation:	
Patent Family:	
Other:	

*************
Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Othor/Engelfy):

This Page Blank (uspto)



# STIC SEARCH RESULT FEEDBACK FORM

#### **Eloadidei**an Ing

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen E01 D86

0	Untary Results access
۶	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention.
Coi	nments:

Drop off or send completed forms to STIC/Biotech-Chem Library Ramsan Bldg.



HIS PACE IS BLANK

```
December 29, 2004, 12:10:41; Search time 61.027 Seconds (without alignments) 58.786 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                         2002273
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                2002273 seqs, 358729299 residues
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                     US-09-823-418-2
50
                                                                                                                                                                                                                                         1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                     Run on:
```

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay30683 Apo-B100					'n	Aaw57207 Apo B 100	Aaw41261 Apolipopr	Aaw96892 ApoB-100	Abj37575 Heparin b	æ	Aaw57209 Apo B 100	Aae14541 Human apo		Aaw64587 Human apo		Abb37687 Peptide #	-	Aar72704 Human apo	Aar34031 Sequence	Adj57400 Human apo	Aay31237 Human Apo	Aaw41262 Apolipopr	Aaw96826 Amino aci	Aau98981 Human apo
g	AAY30683	AAY30682	AAY30686	AAY30687	AAY30685	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826	AAU98981
H	4 7		2 A								2 A			2 A	2 A	2	4		•	•	8 A		•		7. Y
H DB								'n	٠.		~	~	4	9	۲.	.,	·						•	•	
Length	П	Ä	ਜ	ਜ	٦	7		급	Ħ	Ñ	Ċί.	Ċ,	m	ñ	'n	io	343	343	377	377	2463	392	453	4536	456
% Query Match	100.0	92.0	88.0	88.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0
Score	20	46	44	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
Result No.	н	~	m	4	S	9	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Aaw87717 Analogue Aae21732 BSMR effe
ADD48677 AAO15893 ABR40253 ABR40253 ABR43408 ADF43447 ADO33447 ADO33447 AAV30699 AAY30690 AAY30690 AAY30690 AAY30690 AAY30690 AAY30690 AAY30690 AAY30690	AAW87717 AAE21732
\[     L \text{L	12 12
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	11
8866000 88660000 886600000 8866000000000	76.0
₩₩ ₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	38
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 5

## ALIGNMENTS

Apo-B100; proteoglycan receptor mutation, atherosclerosis, low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Š AAY30683 standard; peptide; 10 98US-0077618P. 99WO-US004805. Boren JOS; (first entry) (REGC ) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Synthetic. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999 AAY30683; RESULT 1 AAY30683 

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.

Claim 17; Page 57; 70pp; English.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

Sequence 10 AA;

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which compounds which are method comprises detecting compounds which affect to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which medulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                 ö
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                 ;
0
                                                                                                                                                                       100.0%; Score 50; DB 2; Length 10; 100.0%; Pred. No. 0.0024; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   AAY30682 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                   1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                      TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551509/46.
                                                                                                                                                                                         Local Similarity
les 10; Conserv
                                                                                                                                      Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Innerarity TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9946598-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30682;
                                                                                                                                                                       Query Match
                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                               RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                       8888888888
                                                                                                                                                                                                                                                     ठे
                                                                                                                                                                                                                                                                                      g
```

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from amino acids 3158 to 3167 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (EG). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo sessay methods for identifying compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identify compounds which result in an increase in a particular food or drug composition the assays may be used to determine whether a particular food or drug composition the polynucleotides can also be formation of atherosclerotic lesions. The polynucleotides can also be
                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                      Gaps
                                                                                                                                                                                                                                                                                                                                   Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
Score 46; DB 2; Length 10; Pred. No. 0.016;
                                    0, Indela
                                      1, Mismatches
                                                                                                                                                                                           AAY30686 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 57; 70pp; English.
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0077618P.
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Innerarity TL, Boren JOS;
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                                                                        ||||||:||||
TRLTRERGLK 10
                                                                      1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551509/46.
                  Best_Local Similarity
Matches 9, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9946598-A1
                                                                                                                                                                                                                                                                17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1999.
                                                                                                                                                                                                                             AAY30686;
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
 Query Match
                                                                                                                                                      RESULT 3
                                                                                                   셤
                                                                                                                                                                                                           ð
```

ô

Gaps

ö

Length 10; 1; Indels

DB 2;

88.0%; Score 44; DB 2; 90.0%; Pred. No. 0.04; cive 0; Mismatches

Query Match
Best Local Similarity 90.07

1 TRLTRDRGLK 10

ò

Synthetic.

AAY30687;

셤

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method compouse are detecting compounds which affect to 3367 of apoB100. The method compouse which disrupt LibLp Bolinding with proteoglycan (FG). The method can be used for identifying compounds which disrupt LibLp Bolinding without inhibiting LibL receptor binding Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the captures human apo-B100 can be used as an in vivo model system for the compounds which modulate atherosclerosis and/or LibL-PG binding. They can also be used to identify compounds which result in an increase in absorber to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether can particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                       Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                         Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.0%; Score 43; DB 2; Length 10; 90.0%; Pred. No. 0.065; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0077618P.
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Innerarity TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 AA;
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                     WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1998;
                                                                         17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1999,
                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57205;
                           AAY30685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW57205
     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which andulate atherosaclerosis. The peptides are derived from anino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which distrupt LDL-BG binding without inhibiting LDL receptor binding. Such compounds can be used to the formation of atherosclerotic lesions and prevent reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the cypress human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which result in an increase in also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether formation of atherosclerotic lesions. Thus the assays may be used to determine whether formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                         Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                           Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 10;
Pred. No. 0.04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                             AAY30687 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0077618P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
||||| ||||
TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1998;
                                                                                                                                                                                                                                           17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1999
```

ö

Gaps

.. 0

Apo B binding site peptide 2.

AAY30685 standard; peptide; 10 AA.

RESULT 5
AAY30685
ID AAY3

셤 ઠ

4

us-09-823-418-2.rag

```
RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW41261
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 speptide component that has at least 1 binding site for an apo B protein receptor and at least 1 inpophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with acquences: KAEYKKKHRH (1) or TTRLTRRGLK (2), or their dimers. Nonnaturally occurring, receptor-competent LDL particles are useful as: (i) chug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B specially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B specially as growth and tends to aggregate, to provide binding refinite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
 Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                   Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2; Length 11;
Pred. No. 0.072;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                     Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                    Claim 12; Page 52; 73pp; English.
                                                                                                                            97WO-GB002610.
                                                                                                                                                    96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1998 (first entry)
                                                                                                                                                                          (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
                                                                                                                                                                                                     Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRLTRKRGLK 11
                                                                                                                                                                                                                             WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                          WO9813385-A2
                                                                                                                           25-SEP-1997;
                                                                                                                                                    27-SEP-1996;
                                                                                                  02-APR-1998
                                                                                                                                                                                                   Halbert GW,
                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57207
X L L H X S X & & & X E X L X Y X B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 septide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KAEYKKNKHRH (1) or THRLTRKRGLK (2), or thair dimens. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B protein require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                          peptide binding to apo B protein
delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.0%; Score 43; DB 2; 90.0%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Non-natural lipid particle comprising receptor - useful as, e.g. vector for
                                                                                                                                                                                                                                                                                                     Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 7; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein B-100 fragment.
                                                                                                                    97WO-GB002610
                                                                                                                                                                             96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB001255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96GB-00009702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                      (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                               Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prothrombinase complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
WO9813385-A2.
                                                                                                                 25-SEP-1997;
                                                                                                                                                                             27-SEP-1996;
                                                     02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09743311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW41261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
```

```
RESULT 10
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                    formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-cagulant properties of apolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKRRE-X2-T-Z1 (1) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (aa); Z2 = the C terminus of the peptide a terminal amide group or 1-77 as . Compositions containing the peptide are used for simultaneous, comparate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits activation of the prothrombinase complex; and prevents activation of carriage of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                  apo:lipo:protein B-100 with anticoagulant activity preventing coagulation, inhibiting angiogenesis,
                                                                                                                                                                                                      This sequence is an example of the peptide of the invention. It has the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.0%; Score 43; DB 2; Length 15; 90.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
(UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moore JP;
                                                                                                  Peptide fragments of apo:lipo:proteiused for treating or preventing coageell differentiation and apoptosis.
                                                                                                                                                                      Disclosure; Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW96892 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00874807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoogeveen RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRLTRKRGLK 10
                                                                  WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-070331/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 9; Conserv
                                Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
 8
```

```
ö
                                                                                                                                                     human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein (IDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in viro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
                                                                                                                                  AAW96878-97 represent nuclear localisation signal sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.0%; Score 43; DB 2; Length 15; 90.0%; Pred. No. 0.1; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heparin binding peptide sequence #28.
                                                                                          Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-2002; 2002WO-US023419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2001; 2001US-0306726P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-300420/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETH ZUERICH.
UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003007689-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003.
                                              treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABJ37575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ETHZ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYZU-)
```

Length 22;

```
Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                AAW57209;
                                                                                                    RESULT 12
                                                                                                                AAW57209
                                                                                                                            ઠે
                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 begind at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences KARYKNKHRH (1) or TTRLTRREGIK (2), or their of mers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally accounting, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                  ö
                                                                                                                                                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                    Gaps
                                                                  ;
0
                                           Length 20;
                                                                  1; Indels
                                                                                                                                                                                                                                    Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                    'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                          /note= "attached to cholesterol"
                                            DB 6;
                                           Score 43; DB 6;
Pred. No. 0.14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                    AAW57208 standard; peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Owens MD, Baillie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96GB-00020153
                                           86.0%;
90.0%;
                                                                                                                                                                                                                  03-AUG-1998 (first entry)
                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYST ) UNIV STRATHCLYDE
                                                                                         1 TRLTRDRGLK 10
                                                                                                      7 TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-230637/20.
                                          Query Match
Best Local Similarity
                       Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                               Key
Modified-Bite
                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                               WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halbert GW,
                                                                                                                                                                                                                                                                                                         Synthetic.
 invention
                                                                                                                                                                                           AAW57208;
                                                                 Matches
                                                                                                                                                 RESULT 11
 SXS
                                                                                                                                                                     셤
                                                                                         ઠ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a specifically claimed Apo B 100 binding attempting analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least lesst intention and at least lipophilic substituent. Also described in the invention are peptides containing an apo B binding site for an apo B protein receptor and at least containing an apo B binding sequence with a least invention are peptides containing an apo B binding sequence with a least close in Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-taxgeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives occurring, receptor-competent LDL particles are useful culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 22;
                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "attached to retinoic acid"
Score 43; DB 2;
Pred. No. 0.15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.0%; Score 43; DB 2; Best Local Similarity 90.0%; Pred. No. 0.15; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apo B sequence, which is affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baillie G;
                                                                                                                                                                                                                                                                                                                                   AAW57209 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 7; 73pp; English.
      86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1998 (first entry)
                                                             9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYST ) UNIV STRATHCLYDE.
                                                                                                                        1 TRLTRDRGLK 10
                                                                                                                                                                TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

AAE14541;

RESULT 13

윤

AAE14541

```
AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (ULDL), intermediate density lipoproteins (LDL), low density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to enkaryotic cells, in vivo or in vitro, for expressing a therapeutic polypoptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                           Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus
                     Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.0%; Score 43; DB 2; Length 36; 90.0%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human apolipoprotein peptide fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Fig 12C; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW64587 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                 97US-00874807.
98US-00079030.
                                                                                                                                                                                                                                                                                                                   98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36 AA;
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                             WO9856938-A1.
                                                                                                                                                                                                                                                                                                                   10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                 13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                        17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP857973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW64587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                         Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               samble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and andothalial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apos-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.0%; Score 43; DB 5; Length 34; 90.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.25
0; Mismatches
                                                                                                                                                                                                                                                Human apoB-100 derived peptide p62.
                                                                                                             AAE14541 standard; peptide; 34 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yla-Herttuala S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTRDRGLK 10
7 TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 TRLTRKRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-179777/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200206314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                   peptide p62
                                                                                                                                                                                                     17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Narvanen O,
```

ö

Gaps

.. 0

1; Indels

AAW96876;

XXXX

RESULT 14 AAW96876 ID AAW9

Query Match

8

```
12-AUG-1998,
```

Schenk V;

Lang H,

```
98EP-00890007.
            97AT-00000044.
                      Moritz B, Kiessig S,
                           WPI; 1998-416142/36.
                 (IMMO) IMMUNO AG.
            13-JAN-1997;
       12-JAN-1998;
```

AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain allelss of aposition, which hypercysteinsemia and venous thrombosis) and factor VII mutations (associated with increased risk of daveloping Alzheimer's disease), thermostable 5,10-methylaneterahlydrofolate reductase cased associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method dees not require complex apparatus for polymerase particularly suited to routine screening. It also allows mutant protein a sample to be quantified Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis. Example 2; Page 9; 18pp; German.

Sequence 37 AA;

ö Query Match 86.0%; Score 43; DB 2; Length 37; Best Local Similarity 90.0%; Pred. No. 0.27; Matches 9; Conservative 0; Mismatches 1; Indels

ö

Gabe

1 TRLTRDRGLK 10 ||||| |||| 11 TRLTRKRGLK 20

d ò

Search completed: December 29, 2004, 12:28:47 Job time : 63.0227 secs

```
December 29, 2004, 12:10:41; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                          2002273
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  2002273 segs, 358729299 residues
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                   US-09-823-418-3
48
1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\*

geneseqp2004s:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

A\_Geneseq\_23Sep04:\* 1: geneseqp1980s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

••

Database

SUMMARIES

# ĕ

Description	Aay30684 Apo-B100	Aay30686 Apo-B100					Aaw57207 Apo B 100	Aaw41261 Apolipopr	O	Abj37575 Heparin b	8	Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abg52504 Human liv	Aar72704 Human apo	Aar34031 Sequence	Adj57400 Human apo	Aay31237 Human Apo	N	Aaw96826 Amino aci
ΙD	AAY30684	AAY30686	AAY30685	AAY30682	AAY30687	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826
8	2	~	~	~	N	N	N	~	~	9	~	~	Ŋ	~	~	N	4	4	~	~	8	~	7	7
% Query Match Length DB	10	10	10	10	10	11	13	15	15	20	22	22	34	36	37	51	343	343	377	377	2463	3923	4536	4536
% Query Match	100.0	93.8	91.7	9.68	9.68	9.68	89.6	9.68	9.68	9.68	9.68	89.6	89.6	89.6	9.68	89.6	89.6	89.6	89.6	9.68	9.68	89.6	89.6	9.68
Score	48	45	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
Result No.	1	7	e	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

	Aaols893 Human apo Abr40253 Human ali	Abu79140 Apolipopr	Adf43408 Apolipopr	Adh18871 Human apo	Adh18870 Human apo	Ado33445 Human apo	Ado33447 Human apo	Aau33184 Novel hum	Aay30683 Apo-B100	Aay30690 Apo-B100			Aaw57206 Apo B 100	Aaw87717 Analogue	Aae21732 BSMR effe	Abu07938 Apoprotei	Adf56451 Human apo	Aaw41260 Apolipopr
ADD48677	ABR40253	ABU79140	ADF43408	ADH18871	ADH18870	AD033445	AD033447	AAU33184	AAY30683	AAY30690	AAY30692	AAY30688	AAW57206	AAW87717	AAE21732	ABU07938	ADF56451	AAW41260
561 7	563 6	563	563 7	263	263	563 8	563 8	590 4	10 2	10 2	10 2	10 2	11 2	11 2	11 5	11 6	11 7	12 2
٠	89.6	89.6	89.6	89.6	89.6	89.6	89.6	89.6	87.5	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2
43	4. 4. 2. 6.	43	43	43	43	43	43		42	38	38	38	38	38	38	38	38	38
26	788	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Š Claim 17; Page 57; 70pp; English. AAY30684 standard; peptide; 10 98US-0077618P. 99WO-US004805. Innerarity TL, Boren JOS; (first entry) (REGC ) UNIV CALIFORNIA. WPI; 1999-551509/46. Synthetic. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999 AAY30684; RESULT 1 AAY30684 

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroaclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (BG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroaclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human app-B100 can be used as an in vivo model system for the study of atheroaclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

Aau98981 Human apo

5 AAU98981

4560

9.68

43

25

~

Sequence 10 AA;

S

ö

```
AAY30582-Y30700 represent apo-Bl00 derived peptides showing proteeglycan receptor mutations. They were created to identify compounds which modulate attenoselerosis. The peptides are derived from aminon acids it modulate attenoselerosis. The peptides are derived from aminon acids to a367 of apoBl00. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotis and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can subsorbed to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the confidentian of atherosclerotic lesions. The polymucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                               ô
                                                                                                                                                                                  100.0%; Score 48; DB 2; Length 10;
100.0%; Pred. No. 0.0073;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     AAY30686 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boren JOS;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                 1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                      1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-551509/46.
                                                                                                                                                                                                    Local Similarity
les 10; Conserv
                                                                                                                                               Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Innerarity TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo Bapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY30686;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                      AAY3068
        8888888
                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                    g
```

```
receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which compounds to 3367 of apo8100. The method comprises are detrived from aminon acids 3358 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the composition that the abarticular food or drug composition tends to stimulate or inhibit the composition tends to stimulate or inhibit the composition that the abarticular food or drug composition tends to stimulate or inhibit the composition tends to stimulate or inhibit the composition tends to stimulate or inhibit the composition that the abarticular food or drug composition tends to stimulate or inhibit the composition that the abarticular food or drug composition tends to stimulate or inhibit the composition that the abarticular food or drug composition tends to stimulate or inhibit the c
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
  Score 45; DB 2; Length 10;
Pred. No. 0.03;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                AAY30685 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0077618P.
     93.8%;
                           90.06;
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Innerarity TL, Boren JOS;
Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                            1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9946598-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                  AAY30685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                      RESULT 3
AAY30685
ID AAY30
                                                                                                                                                           g
                                                                                                            ð
```

ö

Gaps

; 0

Length 10; 1; Indels

91.7%; Score 44; DB 2; 90.0%; Pred. No. 0.047; ive 0; Mismatches

Query Match
Best Local Similarity 90.0
Matches 9; Conservative

1 TRLTRARGLK 10

ð

음

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosele-rosals. The peptides are derived from amino acids 3358 to 336 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which result in an increase in also be used to identify compounds which result in an increase in also be used to identify compounds which result in an increase in also be aperticular food or drug composition tends to stimulate or inhibit the compact of a particular food or drug composition tends to stimulate or inhibit the used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                           ypo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                 Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.6%;
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Innerarity TL,
                                                                    17-NOV-1999
                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                WO9946598-A1.
                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                            16-SEP-1999,
                                                                                                                                                                                                                             Synthetic
                            AAY30687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW57205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57205
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from aminon acids 3358 to 3367 of apoBl00. The method compounds which affect low density lipoprotein (LDL) binding with proceedlycan (EG). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-Bl00 can be used as an in vivo model system for the compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identifying compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                  Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion
                                                                                                                                                                                                                                                                        Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.6%; Score 43; DB 2; Length 10; 90.0%; Pred. No. 0.076; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                    AAY30682 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0077618P
                                                                                                                                                                                                                           17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
||||| || |||
TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRLTRERGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                 AAY30682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +
```

```
ö
                                 Gaps
                                   ö
Score 43; DB 2; Length 10;
Pred. No. 0.076;
0; Mismatches 1; Indels
                                                                                                                                                                                       AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                            Apo B binding site peptide 2.
                                                                                                                                                                                                                                                            03-AUG-1998 (first entry)
```

AAY30687 standard; peptide; 10 AA.

RESULT 5 AAY30687 ID AAY3

ð

us-09-823-418-3.rag

```
The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TIRLTRKRGLK (2), or their dimers Nonsequences: KAEYKKNKHRHH (1) or TIRLTRKRGLK (2), or their dimers Nonsequences: KAEYKNKHRHHH (2) or TIRLTRKRGLK (3), or their dimers (3) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                   Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.6%; Score 43; DB 2; Length 11; larity 90.0%; Pred. No. 0.083; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note≕ "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 52; 73pp; English.
                                                                                                                                                                                            97WO-GB002610.
                                                                                                                                                                                                                                96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                    (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                           Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                              WO9813385-A2
                                                                                                                                                                                                                                27-SEP-1996;
                                                                                                                                                      02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW57207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X T T H X S X K K K X B X D X Y X Y X D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARKKAKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer calls that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-coagulant, apolipoprotein B-100, apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14; prothrombinase complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2;
Pred. No. 0.098;
0; Mismatches
                                                                                                                                                                                                                                                                                                                      Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW41261 standard, peptide, 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.68;
                                                                                                                               97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-GB001255,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96GB-00009702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                       (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                   Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 AA;
WO9813385-A2
                                                                                                                           25-SEP-1997;
                                                                                                                                                                                       27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1997;
                                                            02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9743311-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW41261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
8 X C C C C C C C C C C X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ37575
 셤
                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                   This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKHRHS-X2-T-Z2 (I) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or i-47 amino acids as , Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as. Compositions containing the peptide are used for simultaneous, as parter or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-as peptide, inhibits which he prothrombinase complex; and prevents activation of the prothrombinase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollpoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinom; diabetes; arteriosclerosis.
                                                                                           Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.6%; Score 43; DB 2; Length 15; 90.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
(UNLO ) ROYAL FREE HOSPITAL SCHOOL MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore JP;
                                                                                                                                                           Disclosure; Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96892 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00874807
                                Ettelaie C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guevara JG, Hoogeveen RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRLTRKRGLK 10
                                                            WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-070331/06
                              Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

```
AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), intermediate density lipoproteins (VLDL) and lipoprotein a The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in viro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic, antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatroid arthitis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 2;
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hubbell JA, Schoenmakers R, Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heparin binding peptide sequence #28.
                                                                                          Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-2002; 2002WO-US023419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-2001; 2001US-0306726P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-300420/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ETHZ-) ETH ZUBRICH (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003007689-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003.
                                               treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ37575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

o,

Score 43; DB 2; Length 22; Pred. No. 0.17;

89.6**%**; 90.0**%**;

ဖ

```
Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                    AAW57209;
                                                                                                       RESULT 12
                                                                                                                  AAW57209
                                                                                                                             ઠે
                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKKNKRRH (1) or TRAIRKRGIK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives concurring, receptor-competent LDL particles are useful as: (2) drug-targeting vectors for delivering anticancer drugs to courting, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                     ÷
                                                                                                                                                                                                                                                         Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                      Gaps
                                                                    ö
                                          Score 43; DB 6; Length 20;
Pred. No. 0.15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                   /note= "attached to retinoic acid"
                                                                                                                                                                                                                                    Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                           /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                   AAW57208 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Owens MD, Baillie G;
                                                                 .
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Fig 7; 73pp; English.
                                          89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96GB-00020153
                                                                                                                                                                                                               03-AUG-1998 (first entry)
                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYST ) UNIV STRATHCLYDE
                                                                                       1 TRLTRARGLK 10
                                                                                                            7 TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-230637/20.
                                        Query Match
Best Local Similarity
                      Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                               WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halbert GW,
invention
                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                          AAW57208;
                                                                 Matches
                                                                                                                                                                              SXS
                                                                                                            윱
                                                                                       δ
```

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-
taturally occurring, receptor-competent low density lipoprotein (LDL)

particle of the present invention. The LDL particle comprises at least 1

component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKKNKHRH (1) or TRLITKRGEK (2), or thair diments. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally cocurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.6%; Score 43; DB 2; Length 22; Best Local Similarity 90.0%; Pred. No. 0.17; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "attached to retinoic acid"
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baillie
                                                                                                                                                                                                                                                                            AAW57209 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYST ) UNIV STRATHCLYDE.
                                                        1 TRLTRARGLK 10
                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRARGLK 10
                                                                                                                   7 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

AAE14541;

RESULT 13

셤

```
AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
                     Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.6%; Score 43; DB 2; 90.0%; Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human apolipoprotein peptide fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Fig 12C; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW64587 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                       98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                  97US-00874807.
98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guevara JG, Hoogeveen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36 AA;
                                                                                                                                                                                                                               WO9856938-A1
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                       10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                  13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1998
                                                                                                                                                                                                                                                                          17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP857973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW64587
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BXSXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                          Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.6%; Score 43; DB
90.0%; Pred. No. 0.26
:ive 0; Mismatches
                                                                                                                                                                                                                                                  Human apoB-100 derived peptide p62.
                                                                                                          AAE14541 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 90.(
Matches 9; Conservative
7 TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRLTRKRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-179777/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200206314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lipoprotein.
                                                                                                                                                                                                  17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Narvanen O,
```

ö

Gaps ö

25

ઠે

RESULT 14 AAW96876

Query Match

AAW96876;

```
12-AUG-1998
```

```
98EP-00890007.
                               97AT-00000044.
                                                                                        Moritz B, Kiessig S,
                                                                                                                         WPI; 1998-416142/36.
                                                            (IMMO ) IMMUNO AG.
12-JAN-1998;
                             13-JAN-1997;
```

Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis. Lang H,

Schenk V;

Example 2; Page 9; 18pp; German.

AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain alleles of apol indicates increased risk of developing Alzheimer's disease), thermostable 5.10-methylenetetrahydrofolate reductase (associated with hypercysteinaemia and venous thrombosis) and factor VII method can also be applied to proteins from pathogenes, e.g. viruses or prions. The method does not require complex apparatus for polymerase contain reactions, it is simple, standardisable and reliable and is and an almost marrieted. particularly suited to routiving a sample to be quantified

Sequence 37 AA;

Gaps ó 89.6%; Score 43; DB 2; Length 37; 90.0%; Pred. No. 0.28; Live 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0
Matches 9; Conservative

ö

셤 à

Search completed: December 29, 2004, 12:28:48 Job time : 62.0227 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

. ::

December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec

US-09-823-418-3 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 TRLTRARGLK 10 Scoring table: Sequence:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri: piri: piri: piri: PIR 79:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Descrip	abolipoprotein B	apolipoprotein B-1	apolipoprotein B-1	apolipoprotein B -	acetyltransferase,	apolipoprotein B-1	conserved hypothet	hypothetical prote	pyruvate dehydroge	ŪLS6 protein - hūm	hypothetical 34.6	hypothetical prote	hypothetical prote	probable DnaJ prot	probable membrane	apolipoprotein B-1	hypothetical prote	cruciferin 1 precu	probable two-compo	apolipoprotein B-1	hypothetical prote	Na+/K+-exchanging	polyketide synthas	1SU ribosomal prot	hypothetical prote	phosphoadenylyl-su	hypothetical prote	ATO L REGIONAL WENT	1
SUM		832802	LPHUB	C60950	JH0102	G87383	E60950	AH0906	E72514	DEHUPT	C48560	E65112	E85985	B91140	D96795	855958	A60950	D70975	A35540	D83041	JH0101	T32744	T18833	T17409	G90222	H70665	528609	E83363	\$39854	
	DB	2	Н	~	~	~	~	~	N	н	-	-	~	~	~	~	~	~	~	7	~	~	0	N	~	N	ч	~	N	
	ngt	596	4563	269	779	173	275	309	208	388	233	309	309	309	398	171	274	387	509	542	784	829	1049	4613	216	225	232	272	290	
æ	ਨੁਖ਼	89.6	89.6	81.2	81.2	77.1	77.1	75.0	72.9	72.9	70.8	70.8	70.8	70.8	70.8	68.8	68.8	68.8	68.8	68.8	68.89	68.8	68.8	68.8	66.7	66.7	66.7	66.7	66.7	
	Score	43	43	39	39	37	37		35	35	34	34	34	34	34	33	33	33	33	33	33	33	33	33	32	32	32	32	32	
	Result No.	1	71	e	4	Ŋ	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21						27	28	

leucine rich repea	probable aminotran	probable phosphopr	clpx (AF218420) [i	ATP-dependent Clp	probable thiophene	tRNA modification	flagellum-specific	H+-transporting tw	flagellum-specific	H+-transporting tw	DNA repair protein	starch synthase (E	H+-transporting tw	probable ppdK prot	flagellum-specific
T17033	D83057	848288	F97512	AF2731	P97698	AG2924	AE0752	C42364	H90963	B64958	B87455	S40051	A10222	H70538	Н85811
8	~	~	(1	7	N	0	N	N	7	7	0	N	N	N	7
329	390	393	425	425	442	442	456	456	457	457	460	484	484	490	496
66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32

### ALIGNMENTS

opolioprotein B - crab-eating macaque (fragment)

C;Species: Macaca fascicularis (crab-eating macaque)

C;Species: Macaca fascicularis (crab-eating macaque)

C;Species: Macaca fascicularis (crab-eating macaque)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C;Accession: 832802

R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic Biochim. Biophys. Acta 1086, 326-334, 1991

A;Title: Apo B metabolism in the cynomique monkey: evidence for post-transcriptional r A;Reference number: 832802; MUID:92075708; PMID:1742325

A;Accession: 832802

A;Accession: 832802

A;Accession: 832802

A;Residues preliminary

A;Molecule type: mRNA

A;Residues: 1-596 cARP>

A;Residues: 1-596 cARP>

A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301

C;Superfamily: apolipoprotein B

Gaps ö Score 43; DB 2; Length 596; Pred. No. 0.76; 1; Indels 0; Mismatches 89.6%; Query Match Best Local Similarity 90.0 Matches 9; Conservative

ö

원 ઠ

apolipoprotein B-100 precursor - human N.Concains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74 N.Concains: Homo sapiens (man) C.Speciess: Homo sapiens (man) C.Speciess: Homo sapiens (man) C.Speciess: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004 C.Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A2 C.Speciess (man) A278510; A25474; A25267; A25266; A24320; A24684; A23817; A25774; A2 R.Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sc. DNA 6, 363-372, 1987

A;Title: DNA sequence of the human apolipoprotein B gene.
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Roceasion: A27850
A;Roclecule type: DNA
A;Residues: 1-617,'A',619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,
A;Residues: 1-617,'A',619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,
A;References: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:O9UMNO; UNI:
B;Rod J: 5, 3495-3507, 1986
A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: r:
A;Reference number: A31058; MUID:87161758; PMID:3030729
A;Reference number: A31058; MUID:87161758; PMID:3030729
A;Reference number: A31058; MUID:87161758; PMID:3030729
A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA>
A;Residues: 1-11,15-2739,'S',2541-3823,'R', Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC.
Nucleic Acids Res. 14, 7501-7503, 1986

us-09-823-418-3.rpr

```
R;Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E., Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B CDNA. Evidence for more than on A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Accession: A29287
A;Accession: A29287
A;Accession: A29287
A;Residues: 3846-4298 <SHO>
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
B;Pfitzner and Characterization of a human apolipoprotein B 100-speci A;Reference number: A25572; MUID:8776044; PMID:3024665
A;Accession: A25572
A;Molecule type: mRNA
A;Residues: 4219-4337, S', 4339-4563 <PFI>A;Coss-references: GB:M36676
B;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
Broc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
A;Reference number: A24738; MUID:86042646; PMID:2932736
A;Accession: A24738; MUID:86042646; PMID:2932736
A;Accession: A24738; MUID:86042646; PMID:2932736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 'N', 3729-3731,'I', 3733-3875,'A', 3877-3948,'F', 3950-3963,'Y', 3965-3982,'S', 391
A; Createrences: GB: M12413; NID: g178735; PIDN: AAAS1742.1; PID: g178736
B; Chen, S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cail
Science 238, 363-366, 1987
A; Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
A; Reference number: A40133; MUID: 88018019; PMID: 3659919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. Accession: B40133
A. Molecule type: mRNA
A. Molecule type: mRNA includes the stop codon of the organ-specific mRNA for apo48
A. Accession: A40133
A. Accession: A40133
A. Molecule type: protein
A. Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55;
A. Molecule type: protein
A. Residues: 51-75;101-110;129-139;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-
B. Hardman, D.A.; Protter, A.A.; Schilling, J. W.; Kane, J.P.
B. Biochem: Biophys. Res. Commun. 149; 1214-1219, 1987
A. Molecule type: protein analysis of human B-48 protein confirms the novel mechanism protein and A28002; MUID: 88106542; PMID: 3426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 2169-2179
A; Molecule type: mRNA
A; Residues: 2169-2179
A; Mote: the sequence shown represents the carboxyl end of apolipoprotein B-48
A; Mote: two RNA species hown represents the carboxyl end of apolipoprotein B-48
A; Mote: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest chencedes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA, R; Asang, n. W.; Lee, B.; Yang, M.; Gotto Jr., A.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A; Reference number: A35783; MUID:90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: mRNA
A, Readudes: 1219-2179, 2181-2235 < HA2>
A, Readudes: 1219-2179, 2181-2235 < HA2>
A, Cores references: GB:M18471
A, Experimental source: intestine
A, Molec: this mRNA from intestine includes a stop codon created by RNA editing in place
R, Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.P.; Kirchgessner,
Nucleic Acids Res. 13, 6937-6953, 1985
A, Title: Human apolipoprotein B: identification of cDNA clones and characterization of
A, Reference number: A24269; MUID:86041888; PMID:3903660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stop codon in human intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 3056-3159 <MEH>
A; Residues: 2056-3159 <MEH>
A; Crose references: GB:X33045; NID:928783; PIDN:CAA26850.1; PID:9929609
R; Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.
Biochem. Blophys. Res. Commun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in
A; Reference number: A29659; MUID:88049670; PMID:2445342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A29659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A231, A24, A251, A251,
                                                                                                                                                           A; Molecula type: mRNA
A; Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'
A; Cross-references: GB:XX04506; NID:934330; PIDN:CAA28191.1; PID:934331
R; Law, S.W.; Grant, S.W.; Higuenti, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID:87041416; PMID:3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-617, A', 619-703, 'P', 705-792, 'R', 794-1270,'S', 1272-1866,'G', 1868-2036,'N', 2
4189-4220,'M', 4222-4563 < LAM>
A; Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
R; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID:87008488; PMID:3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-97, 1', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-
9-4112, 'G', 4134-4180, 'E', 4182-4563 - CHE>
A; Cross-references: GB: J02610; NID: 9178803; PIDN: AAA35549.1; PID: 9178804
A; Cross-references: GB: J02610; NID: 9178803; PIDN: AAA35549.1; PID: 9178804
B; More a: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
B; More a: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
B; Marcher, A.A.; Hardman, DA.; Sato, W.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H
Proc. Natl. Acad. Scl. U.S.A. 83, S678-5682, 1986
A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,MOLECULE TYPE: MENA
A,Residues: 1-97,'I',99-617,'A',619-941,'YYIWSLPPKP',951-1138,'PTGRLPNCFSNGLICYSLWLHSFOR
A,Residues: 1-97,'I',99-617,'A',619-941,'YYIWSLPPKP',951-1138,'PTGRLPNCFSNGLICYSLWLHSFOR
A,Rocenser-references: GR M4081, NID:9178795, PIDN:AAA31752.1; PLD:9553189
R,Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A,Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A,Reference number: A24684; MUID:86094221; PMID:3001697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: mRNA, A Molecule type: mRN2480; NID:9178791; PIDN:AAAS1751.1; PID:9178792
R) Forotter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Killer, Matl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A) Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr A; Reference number: A94088; MUID:86149325; PMID:3513177
A;Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A;Reference number: A93639; MUID:87016385; PMID:3763409
```

ŌĒ

m

```
Ciperions and a second a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: apoB
C;Superfamily: apolipoprotein B
C;Superfamily: apolipoprotein B
C;Reywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Getyltransferase, GNAT family [imported] - Caulobacter creecentus
Cispecies: Caulobacter creecentus
Cispecies: Caulobacter creecentus
Cispecies: Caulobacter creecentus
Cispecies: Caulobacter creecentus
Cipace: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
CiAccession: G87383
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haff, D.H.; Kolo,
I, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
J, Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87383
A;Accession: G87383
A;Residues: 1-173 <STO>
A;Residues: 1-173 <STO
A;Residues: 1-173 <STO>
A;Residues: 1-173 <STO
A;Residues: 1-174 <STO
A;Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9A9B1; GB:AE005673; NID:g13422385; PIDN:AAK23067.1; GSPDB:C
C;Genetics:
A;Gene: CC1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apolipoprotein B-100 - chicken (fragment)
(Species Gallus gallus (chicken)
(Species 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
(Staccession: B60950
(Stack A.; Scott, J.
J. Scott, J.
J. L109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 2;
Pred. No. 6.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.1%; Score 37; DB 88.9%; Pred. No. 4; ive 0; Mismatches
                                                                              (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.2%;
                                                                  apolipoprotein B - golden hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.1
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642 SRLTRKRGLK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 TRLMRARGL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLTRARGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                        A;Modecule type: protein
A;Modecule type: protein
A;Modecule type: protein
A;Modecule type: protein
A;Accession: 82066
A;Modecule type: protein
A;Accession: 82066
A;Modecule type: protein
A;Accession: 82066
A;Modecule type: protein
A;Modecular type: protein
A;Modecula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apolipoprotein B-100 - golden hamster (fragment)
C.Species: Mesocricetus auratus (golden hamster)
C.Species: Mesocricetus auratus (golden hamster)
C.Species: J1-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Accession: C60950
R.Law, A., Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A.7ttle: A cross-species comparison of the apolipoprotein B domain that binds to the LDL A.Reference number: A60950; MUID:90324804; PMID:2373961
A.Reference number: A60950; MUID:90324804; PMID:2373961
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-269 - LLAW>
A.Residues: 1-269 - LLAW>
A.Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C.Superfamily: apolipoprotein B
C.Superfamily: apolipoprotein B
C.Superfamily: apolipoprotein; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                  9
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.B.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS. Lett. 170, 105-108, 1984
A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Title: Human apolipoprotein B: Pattial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.6%; Score 43; DB 1; Length 4563; 90.0%; Pred. No. 5.2; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

81.2%; Score 39; DB 2; Length 269;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3385 rkirkkkcik 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||| ||||
216 SRLTRKRGLK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                          A; Accession: A22006
```

a

ઠે

ö

Gaps ö

Indels

ö

Gaps

ö

RESULT

셤

ઠ

```
A;Genee: GDB:PDHA2
A;Genee: GDB:PDHA2
A;Genee: GDB:PDHA2
A;Genee: GDB:PDHA2
A;Genee: GDB:COSS-references: GDB:120711; OMIM:179061
A;Map position: 4922-4923
G;Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin C;Keywords: flavoprotein; heteroterramer; mitochondrion; oxidoreductase; phosphoprotein.
F;18-230/Forduct: pyruvate dehydrogenase (lipoamide) alpha chain #status predicted <MAT>F;183-232/Domain: thiamin pyrophosphate-binding domain homology <TPB>F;230/Binding site: phosphate (Ser) (covalent) #status predicted
F;230/Rinding site: phosphate (Ser) (covalent) #status predicted
F;298/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                             pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain precursor, testis-specific -
N.Alternate names: pyruvate dehydrogenase complex, El component alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Homo maples (man)
Cispecies: Homo maples (man)
Cipate: 31.Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
Cipate: 31.Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
Cipate: 31.Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
Ribahl, H.H.M.; Brown, R.M.; Hutchison, W.M.; Maragos, C.; Brown, G.K.
A; Dachonics 8, 225-232, 1990
A; Title: A testis-specific form of the human pyruvate dehydrogenase Elalpha subunit is A; Reference number: A37104; MUID:91065637; PMID:2249846
A; Accession: A37104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-388 <DAH>
A;Cross-references: UNIPROT:P29803; GB:M86808; GB:J04769; NID:g190789; PIDN:AAA60232.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Accession: C48560
R, Rosen-Wolff, A.; Frank, S.; Raab, K.; Moyal, M.; Becker, Y.; Daral, G.
Nyirus Res. 25, 189-199, 199, 199,
A, Title: Determination of the coding capacity of the BamHI DNA fragment B of A, Reference number: A48560; MUID:93070559; PMID:1332274
A, Recession: C48560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: human herpesvirus 1
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: DNA
A;Residues: 1-233 <ROS>
A;Residues: U-233 <ROS>
A;Cross-references: UNIPROT: P36297
A;Note: sequence extracted from NCBI backbone (NCBIN:117573, NCBIP:117577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaрв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.9%; Score 35; DB 1; Length 388; 80.0%; Pred. No. 22; 21ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.8%; Score 34; DB 1; Length 233; Best Local Similarity 100.0%; Pred. No. 22; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UL56 protein - human herpesvirus 1 (strain HFEM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: UL56
C;Superfamily: herpesvirus UL56 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                  165 RLARARGVK 173
                                                                      2 RLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVLTRAEGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 RLTRARG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLTRARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
E65112
                                                                      ò
                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica (5.8pecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (5.Accession: AH0906 R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Cunnerton, P.; Cronin, A.; Davis, P.; Daviss, R.M.; Dowd, L.; White, N.; Farrar, t.; Moule, S.; O'Gacra, P. Davis, P.; Daviss, R.M.; Dowd, L.; White, N.; Farrar, Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Atleic Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Accession: AH0906 A;Stetus: preliminary A;Molecule type: DNA A;Reterences: GB:AL513382; PIDN:CAD07846.1; PID:g16504394; GSPDB:GN00176
                             A/Accession: E60950
A/Molecule type: mRNA
A/Molecule type: TS < LAM>
A/Molecule type: TS < LAM>
A/CESSION TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9YA48; DDBJ:AP000063; NID:g5105654; PIDN:BAA81101.1; PID:g5
A;Experimental source: strain K1
C;Genetics:
A;Gene: Asiono: Aigene Aigene: C;Superfamily: dTMP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein APE2090 - Aeropyrum pernix (etrain K1)
C.Species: Aeropyrum pernix
C.Species: Aeropyrum pernix
C.Species: Aeropyrum pernix
C.Accession: E72514
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah War, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takah DNA Res
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUD:99310339; PMID:10382966
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                 Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.0%; Score 36; DB 2; Length 309; Best Local Similarity 70.0%; Pred. No. 11; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: STY3508
C;Superfamily: Methanococcus jannaschii conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
A, Reference number: A60950, MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                         77.1%; Score 37; DB 2;
80.0%; Pred. No. 6.3;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.9%; Score 35; DB Best Local Similarity 77.8%; Pred. No. 12; Matches 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 İSLİRKRGİK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||: | ||||
TRIARERGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: dTMP kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-208 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

Ŋ

```
C;Keywords: transmembrane protein
F;24-40/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: MIPS:YLR402w
A,Cross-references: SGD:S0004394
A,Map position: 12R
C,Superfamily: Saccharomyces pro)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 TQLARQRGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 rkakcik 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-398 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: F28016.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Du, Z
                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                    C; Accession: E65112
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: E65112
A; Accession: E65112
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-309 cBLAT>
A; Residues: 1-309 cBLAT>
A; Cross-references: UNIPROT:P45476; GB:AB000400; GB:U00096; NID:g2367203; PIDN:AAC76243.
A; Experimental source: strain K-12, substrain MG1655
C; Genetics:
A; Gene: yhcC
C; Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Accession: B85985
R. Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew B.; Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grobeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N. Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A, Reference number: A88480; MUD:21074935; PMID:11206551
A, Refatus: Preliminary
A, Reference number: A88480; MUD:21074935; PMID:11206551
A, Residues: DNA
A, Residues: 1-309 < ATO-
A, Cross-references: UNIPROT:P45476; GB:AE005174; NID:g12517832; PIDN:AAG58345.1; GSPDB:GGenetics: 1-309 < ATO-
A, Experimental source: strain O157:H7, substrain EDL933
C, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein yhcC [imported] - Bacherichia coli (strain 0157:H7, substrain EDL93
C;Species: Bacherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bscherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: B91140

C;Accession: B91140

C;Accession: B91140

B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gency

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: B91140

A;Accession: preliminary

A;Accession: Bylay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein EC84090 [imported] - Escherichia coli (strain O157:H7, substrain R1
hypothetical 34.6 kD protein in arcB-gltB intergenic region - Escherichia coli (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                  C'Species: Escherichia coli
C'Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 1; Length 309;
Pred. No. 29;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.8%; Score 34; DB 2; Length 309; 70.0%; Pred. No. 29; cive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.8
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 TOLARORGIK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| | ||||
170 TQLARQRGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
A;Cross-references: UNIPROT:P45476; GB:BA000007; PIDN:BAB37513.1; PID:g13363563; GSPDB:c
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Genetics:
C;Genetics:
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable DnaJ protein, 19794-17391 [imported] - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: OZ-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C'Accession: D95795
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Titles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D95795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9SRE3; GB:AE005173; NID:g6143904; PIDN:AAF04450.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S55958
A;Molecule type: DNA
A;Residues: 1-171 cDUZ.
A;Fesidues: 1-171 cDUZ.
A;Cross-references: UNIPROT:006057; EMBL:U19729; NID:g625097; PID:g625102; GSPDB:GN0001
A;Experimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: hypothetical protein L8084.5
C;Species: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: 855958
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable membrane protein YLR402w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                    2; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 398;
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YLR402w
                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, January 1995
A;Description: The sequence of S. cerevisiae cosmid 8084.
A;Reference number: 855944
                                                                                                                                                                                                                                 Score 34; DB
Pred. No. 29;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.8%; Score 34; DB 100.0%; Pred. No. 37; ive 0; Mismatches
```

```
F;130-146/Domain: transmembrane #status predicted <TM2>
```

TRLTRARG 8	TRLRRARG 86
••	7.
ò	qa
	Qy 1 TRITRARG 8

Search completed: December 29, 2004, 12:39:01 Job time : 11.6591 secs

Q9ya48 geropyrum p Q8duw3 streptococc Q746g7 thermus the A882418 thermus the Convact homo sapien Genraci homo sapien Aah66953 homo sapien Q8ixg plasmodium Q8ixg coryrebacte Q8iag plasmodium Q8ixg plasmodium Q8ixg plasmodium

Aas04184 mycobacte Q8ij19 plasmodium

Sequence:

Run on

Searched:

Database

Result ŝ 

```
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-2761261.

Amrine-Madesn H., Koepfli K.-P., Wayne R.K., Springer M.S.;

Amrine-Madesn H., Koepfli K.-P., Wayne B.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AF548396; AAP97352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apolipoprotein B (Fragment).
Macaca fasticularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45955 MW; EEFA8492157E1BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2
Pred. No. 2.9;
0; Mismatches
                                                                                                                                                                                                                        414 AA
                                                                                                                                                                     ALIGNMENTS
073YT8

081J19

081J19

081J19

040UW3

0746G7

00PT HUMAN

00NY HUMAN

00NY HUMAN

00NY HUMAN

00NY HUMAN

00NY GORY O
                                                                                                                                                                                                                                                                         Apolipoprotein B 100 (Fragment).
Name=apoB-100,
Aotus vociferans (Spix's owl monkey).
                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                          (TrEMBLrel. 25, C
(TrEMBLrel. 25, L
(TrEMBLrel. 25, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.6%;
                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
 2073
2073
158
208
208
208
208
365
365
403
403
600
600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 TŘĽTŘKŘĠĽK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein.
NON TER
NON TER 41
SEQUENCE 414
                                                                                                                                                                                                                                  Q7YQR5;
01-OCT-2003 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                01-OCT-2003
  Q28473
Q28473;
                                                                                                                                                                                                                        Q7YQR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
 Q7YQR5
                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O72600 homo sapien
O72600 homo sapien
O7716 diceros bic
O7940 diceros bic
O7940 prescopus by
O7104 rousettus a
O7970 chaetophrac
O71164 agouti paca
O7111 hydrochoeru
O7117 hydrochoeru
O7117 hydrochoeru
O6053 mesocricetu
O6053 mesocricetu
O6053 mesocricetu
O6053 mesocricetu
O6053 mesocricetu
O6030 mesocricetu
O6030 mesocricetu
O6030 mesocricetu
O6030 mesocricetu
O6030 mesocricetu
O7017 gallus gall
O77400 tachyglossu
O77400 dinomys bra
O77400 dinomys bra
O77400 dinomys bra
O97940 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              salmonella
atherurus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                         macaca fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hystrix bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       salmonella
                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                      December 29, 2004, 12:13:11; Search time 58.4091 Seconds (without alignments) 98.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homod
                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7cpn5
Q7tn65
Q7tn69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8xfv9
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q28473
Q13788
APB HUMAN
Q7Z600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7TN72
Q60536
Q60537
Q6NAC6
CAE26702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7YR10
Q7YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7YQM7
Q7YR04
Q7YR08
Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7YQN0
Q7TN70
Q9FXM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7CPN5
Q7TN65
Q7TN69
                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9LVA4
Q8XFV9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7TN68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27YQN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27YOM9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29A9B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRIBTO
                                                                                                                                                                                                                                                                                                        UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                          BB
                                                                                                                  US-09-823-418-3
                                                                                                                                   TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445
445
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       400
                   Copyright
                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                             Perfect score:
```

ö

Gaps

.

2; Length 414;

ä

```
Wed Dec 29 15:38:58 2004
```

Best Loc Matches

ð 유

RESULT 3

```
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          Nucleic Acids Res. 14:7501-7503(1986)
                                                                                                                                                                                                                                                                                                                 Biol. Chem. 261:12918-12921(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=87161758; PubMed=3030729;
                                                                                                                                                                                                                 DNA 6:363-372(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zannis V.I
         OC
RELIEF BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER
BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER
                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87191999; PubMed=2883086;
Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
Analysis of the human apolipoprotein B gene; complete structure of the B-74 region.";
Gene 49:29-51(1986).
BEMBL; M15421; AAA51758-1; -.
PIR; A27850; LPHUB.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0005519; F:lipid transporter activity; NAS.
NON_TER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APB_HUMAN STANDARD, PRT; 4563 AA.
P04114; 000502; Q13787;
01-N0V-1986 (Rel. 03, Created)
01-N0V-1986 (Rel. 03, Last sequence update)
05-UUL-2004 (Rel. 44, Last sequence update)
Apollboprocein B-100 precursor (Apo B-100) [Contains: Apollpoprotein Name-APOB;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
"Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991).
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                               Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 3262;
                                                                                                                                                                                                                      1; Indels
                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56603BC0618DD40D CRC64;
                                                                                                                                                      596 596
596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                           Score 43; DB 2;
Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                     PRT; 3262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370140 MW;
                                                                                                                                                                                           89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.6%;
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                   EMBL, X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                                                     9; Conservative
                                                                         Murray R.;
Submitted (FEB-1992) to
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2084 TRLTRKRGLK 2093
                                                                                                                                                                                                                                                                    226 TRLTRKRGLK 235
                                                                                                                                                                                                                                           1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                  APOB protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Congery
                                                                                                                                            1
596
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                            Lipoprotein.
NON TER
NON TER 59
                                                               TISSUE=Liver;
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE
                                                                                                                                                                                                                                                                                                                                   Q13788
Q13788;
```

Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

RESULT 4
APB\_HUMAN

OSSEEDTAGE

셤 ò

SEQUENCE OF 3109-4563 FROM N.A.
MEDLINE-85300528; PubMed=2994225;
Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.P., Urdea M.S., Lavy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M., Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B., Mahley R.W., Scott J.;
"Human apolipoprotein B: structure of carboxyl-terminal domains, sites of gene expression, and chromosomal localization."; "The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986). [3]
SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE-8708488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-SEQUENCE OF 3056-3159 FROM N.A.
MEDLINE=86041888; PubMed=3903660;
Mehrablan M., Schumaeker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNA.";
Nucleic Acids Res. 13:6937-6953(1985). SEQUENCE FROM N.A.
MEDLINE=87016385; PubMed=3763409;
MEDLINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181. MEDLINE-86093680; PubMed-3841204; Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O., SEQUENCE FROM N.A.
MEDLINE=87041416; PubMed=3464946;
MEDLINE=87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.;
Lee N., Brewer H.B. Jr.;
"Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
derived amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986). Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier (Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J., "DNA sequence of the human apolipoprotein B gene."; Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D., Bjursell G.; "Molecular cloning of human apolipoprotein B cDNA."; Nucleic Acids Res. 13:8813-8826 (1985). В. П [6]
SEQUENCE OF 709-906 FROM N.A.
MEDLINE-85270450; PubMed=3860836;
Deeb S.S., Motulsky A.G., Albers J.J.;
"A partial cDNA clone for human apolipoprotein B
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985) SEQUENCE FROM N.A., AND VARIANT GLU-4181. MEDLINE=88003974; PubMed=3652907;

```
VARIANT LEU-2739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         009240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7Z600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
Q7Z600
          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                       MEDLINE=86149325; PubMed=3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kireher S.W., McEnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L., Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.", Nature 323:738-742(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100.";
Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-848.
MEDLINE=88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.,
"Apolipoprotein B-48 is the product of a messenger RNA with an organ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr., Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R., Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete protein sequence and identification of structural domains of human apolipoprotein B.";
Nature 323:734-738(1986).
                                                                                                                                                                                              SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE-86287319; PubMed-3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of cDNA clones encoding the entire B-26 region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.; "Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene."; Hum. Genet. 86:91-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20143590; PubMed=10679026; Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.,; Parlanton of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALCIUM-BINDING DATA.
MEDLINE=86442245; PubMed=3087360;
Babti N., Lee D.M., Mok T.;
"Apolipoprotein B is a calcium binding protein.";
Biochem. Biophys. Res. Commun. 137:493-499(1986).
                                                                                                                            apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                                                                                                                                                                apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Cell 11:721-734(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT SER-4338.
MEDLINE=91071750; PubMed=1979313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT FDB GLN-3527.
MEDLINE=89098975; PubMed=2563166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in-frame stop codon.";
SEQUENCE OF 1-291 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 238:363-366(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALMITOYLATION OF CYS-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               triglycerides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAINS.
  REPRESENTED FOR THE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SE
```

```
Gaps
                                                                                                             VARIANT FDB CYS-3558.
MEDLINE=95190020; PubMed=7883971;
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,
Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
"Familial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
                                                                                                                                                                                                                                                                                                  VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
                                                                                                                                                                                                                                                                                                                                          MEDLINE=97044521; PubMed=8889592;
Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
MEDLINE=91016974; PubMed=2216805; Manang L.-S., Gavish D., Breslow J.L.; Sequence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS FDB GLN-3527 AND CYS-3558.
MEDLINE=97403938; PubMed=9259199;
Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
Krempf M., Giraudet P., Junien C., Boileau C.,
"Familial ligand-defective apolipoprotein B-100: simultaneous
detection of the ARG3500-->GLN and ARG351-->CYS mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A.,
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Apolipoprotein B (Including Ag(X) antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 36;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.6%; Score 43; 90.0%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                     Clin. Invest. 95:1225-1234(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fum. Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR-SSCP.";
Hum. Mutat. 8:282-285(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 25, CTEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003
01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=APOB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
```

ö

```
Mol. Phylogenet. Evol. 28:225-240(2003)
EMBL; AY243375; AAP50763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=48988;
                              Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
NON TER
NON TER
SEQUENCE 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=apoB-100;
                                                NON TER
SEQUENCE
                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                     Q7YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7YQM7
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7YQM7
           SO FIT SO
                                                                                                                                                                                      셤
                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                 01-0CT-2003 (TrENBLrel. 25, Created)
01-0CT-2003 (TrENBLrel. 25, Last sequence update)
01-0CT-2003 (TrENBLrel. 25, Last annotation update)
40-0CT-2003 (TrENBLrel. 25, Last annotation update)
Glaucomys volans (Southern flying squirrel).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                           MEDLINE-22761261; PubMed=12878460; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; An new Phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships "; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apolipoprotein B (Frament).
Diceros bicornis (Black rhinoceros).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Perissodactyla; Rhinocerotidae; Diceros.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22761261; PubMed=12878460; Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.; "A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                             Score 43; DB 2; Length 4563;
Pred. No. 36;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Match 81.2%; Score 39; DB 2; Length 421; Local Similarity 80.0%; Pred. No. 20; Lonservative 1; Mismatches 1; Indels
                                                                                      4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           421 421
421 AA; 46747 MW; D47B77BD4F864FD1 CRC64;
OTKIO PRELIMINARY, PRT; 432 AM.
OTKIO,
01-OCT-2003 (TERMELRE1. 25, Created)
01-OCT-2003 (TERMELRE1. 25, Last sequence update)
01-OCT-2003 (TERMELRE1. 25, Last annotation update)
                                                                                                                                                                                                                       421 AA
                                                                                                                                                                                                                      PRT;
                                                                                                           89.6%;
                                                                                                Query Match
Best Local Similarity 90.0
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                  3385 TRLTRKRGLK 3394
                                                                                                                                                1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|||| ||||
264 SRLTRKRGLK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       Glaucomys.
NCBI_TaxID=64683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                               Lipoprotein.
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                         Lipoprotein.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                   07TN68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
  윱
                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nyctimene albiventer (Common tube-nosed fruit bat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
Pteropodinae, Nyctimene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-22761261; PubMed=12878460;
Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pteropus hypomelanus (Small flying fox).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                      81.2%; Score 39; DB 2; Length 492;
80.0%; Pred. No. 21;
.ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.2%; Score 39; DB 2; Length 436;
80.0%; Pred. No. 21;
iive 1; Mismatches 1; Indels
432 432
432 AA; 48171 MW; F27B7AB39604732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 436
436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AA
                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last seq
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                         Query Match
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 80.0
                                                                                                                                                                                                                   275 SŘLTŘKŘGĽK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                    1 TRLIRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||| ||||
279 SRLTRKRGLK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pteropodinae, Pteropus.
NCBI_TaxID=9405;
```

ö

Gaps

ö

SO FT FO

ઠે 셤

```
SEQUENCE FROM N.A.

MEDLINE-2761261, bubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22761261; PubMed=12878460;
MEDLINE=22761261; PubMed=12878460;
Marine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
Amine-Madsen H., Koepfil K.-P., Wayne R.K., Springer Compelling whylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
evidence for eutherian relationships.";
EMBL, A7243369; AAPSO757.1;
InterPro; IPR000871; Beta_lactamase_A.
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                             Agouti paca (Paca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apolipoprotein B (Fragment).
Hydrochoerus hydrochaeris (Capybara) (Carpincho).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Hydrochaeridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.2%; Score 39; DB 2; Length 445; 80.0%; Pred. No. 21; 1; Indels :ive 1; Mismatches 1; Indels
                                     2; Length 445;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 1
445 445
445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;
 445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 445 445 445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 AA
                                   81.2%; Score 39; DB 80.0%; Pred. No. 21;
                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                             Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein B (Fragment)
                Query Match
Best Local Similarity 80.00
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                               :|||| ||||
288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 SRLTRKRGLK 297
                                                                                                         1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=108852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrochaeris.
NCBI_TaxID=10149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein.
NON TER
NON TER
SEQUENCE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
NON TER
SEQUENCE
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                      Q7TN64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07TN71
                                                                                                                                                                                                                                     Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                      Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07TN71
 g
                                                                                                                                             셤
                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AX243383; AAP50771.1;
                                                                                                                                                                                                                                                                                                                                                                        Apolipoprotein B (Fragment).
Rousettus amplexicaudatus (Common rousette).
Rusettus amplexicaudatus (Common rousette).
Ruservota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae; Pteropodinae; Rousettus.
NCBI_TaxID=58083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Bvol. 28:225-240(2003).
EMBL; AX243378; AAP50766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
1-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
4pollpoprotein B (Fragment).
Abollpoprotein B (Fragment).
Chaetophractus villosus (South American armadillo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                       Score 39; DB 2; Length 438;
Pred. No. 21;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.2%; Score 39; DB 2; Length 438; 80.0%; Pred. No. 21; 1; Mismatches 1; Indels
                                                438
48734 MW; 2BD85BCBF4B2CC41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48597 MW; 41C890DEAF95C872 CRC64;
                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                          438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                         81.2%;
80.0%;
EMBL; AF548436; AAP97392.1;
                                                                                                     Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                   :|||| ||||
281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||| ||||
281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1438
                                                                                                                                                                              1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRARGLK 10
                                   1
438 4
438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein.
NON TER
NON TER 4
                  Lipoprotein.
NON TER
NON TER 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                          Q7YR04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7YR08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
```

Q7YR08

8 g

ö

Gaps

```
셤
                                                   ö
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                              01-077-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment)
Erethizon dorsatum (North American porcupine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Erethizontidae;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolitoprotein B, provides compelling wol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243368; AAP50756.1; -.

Lipoprotein. 1

NON TER 145 445

SEQUENCE 445 AA; 49617 MW, 9572FB5FB5E7625F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=90236327; PubMed=2332175;
Smith T.J., Hautamaa D., Mada N.;
"Sequence of the putative low-density lipoprotein receptor-binding cedons of apolipoprotein B in mouse and hamster.";
regions of apolipoprotein B in mouse and hamster.";
EMBL, M35187; AAA37059.1; -.
EMBL, M35187; AAA37059.1; -.
PIR; C60950; C60950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OG0536 PRELIMINARY; PRT; 780 AA.
060536 (TEMBLE). 01, Created)
01-NOV-1996 (TEMBLE). 01, Last sequence update)
01-NOV-1996 (TEMBLE). 01, Last sequence update)
Hamster apolipoprotein (appo) (Fragment).
Hamster apolipoprotein (appo) (Fragment).
Mesocricetus auratus (Golden hamster).
Mesocricetus Autatus (Golden hamster).
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Score 39; DB 2; Length 445;
Pred. No. 21;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%; Score 39; DB 2; Length 445; 80.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 445
445 AA; 49617 MW; 9572FE5F5E7625F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            780 780
780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
                                                                                                                                                           445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                           PRT;
Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 80.0
                                                                        :|||| ||||
288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||| ||||
288 SRLTRKRGLK 297
                                                    1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=34844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein.
NON TER
NON TER
76
SEQUENCE 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                       Q7TN72;
                                                                                                                                                       Q7TN72
                                                                                                                          RESULT 14
Q7TN72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                g
                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

```
ö
                                     Gaps
                                   ç
O
    81.2%; Score 39; DB 2; Length 780; 80.0%; Pred. No. 38;
                                   1; Indels
                                1; Mismatches
Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                          :|||| ||||
642 SRLTRKRGLK 651
                                                          1 TRLTRARGLK 10
```

Search completed: December 29, 2004, 12:37:30 Job time : 59.5202 secs

```
December 29, 2004, 12:10:41; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                         2002273
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  2002273 segs, 358729299 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_23Sep04:*

1: geneseqp1980s:*

2: geneseqp21990s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2003as:*

7: geneseqp2003as:*

8: geneseqp2003as:*
                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                  US-09-823-418-4
49
1 TRLTRTRGLK 10
                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                          Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

lon	Apo-B100	Apo-B100	Apo-B100	Apo-B100	Apo-B100	Apo-B100	Apo B bin	Apo B 100	Apolipopr	ApoB-100	Heparin b	Apo B 100	Apo B 100	Human apo	Nucleic a	Human apo	Nucleic a	Peptide #	Human liv	Human apo	Sequence	Human apo	Human Apo	Apolipopr	Amino aci
Description	Aay30685	Aay30686	Aay30684	Aay30683	Aay30682	Aay30687	Aaw57205	Aaw57207	Aaw41261	Aaw96892	Abj37575		Aaw57209	Aae14541	Aaw96876	Aaw64587	Aaw96845	Abb37687	Abg52504	Aar72704	Aar34031	Adj57400	Aay31237	Aaw41262	Aaw96826
QI	AAY30685	AAY30686	AAY30684	AAY30683	AAY30682	AAY30687	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826
08	~	~	~	~	~	~	~	N	~	~	9	~	~	ഗ	~	~	~	4	4	~	~	œ	~	~	7
% Query Match Length DB	10	10	10	10	10	10	11	13	15	15	20	22	22	34	36	37	21	343	343	377	377	2463	3923	4536	4536
% Query Match	100.0	91.8	89.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8
Score	49	45	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
Result No.	Н	7	٣	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aau98981 Human apo Aad48677 Human Pro Aa015893 Human apo Abr40253 Human ali Abu79140 Apolipopr Adf18871 Human apo Ad033447 Human apo Ad033447 Human apo Ad033447 Human apo Ad033497 Human apo Aa03349 Novel hum Aay30690 Apo-B100 Aay31699 Apo-B100 Aay31698 Apo-B100 Aay31698 Apo-B100 Aaw87717 Analogue Aae21732 BSMR effe Abu07938 Apoprotei Adf56451 Human apo	VENTS				proteoglycan receptor mutation.	on; atherosclerosis; LDL; atherosclerotic lesion.									binding of low density lipoprotein obtaining compounds for reducing		on derived peptides showing proteoglycan sated to identify compounds which stifted are derived from amino acids 3358 comprises detecting compounds which affect. Inding with proteoglycan (PG). The method sounds which disrupt LDL-PG binding binding. Such compounds can be used to of atherosclerotic lesions and prevent non-human animals and mammals which non-human animals and mammals which is assay methods for identifying it vivo assay methods for identifying iclerosis and/or LDL-PG binding. They can
AAU98981 Abol5893 Abol5893 Abr40253 Abr79140 Abr73408 Abo33445 Abo33445 Abo33445 Abo33445 Abo3348 Abo33690 Aby30692 AAY30692 AAY30692 AAY30692 AAY30693 AAY30693 AAY30698 AAW87717 ABW87717 ABW87717 ABW87717 ABW87717 ABW87717	ALIGNMENT	10 AA.			showing a pro	receptor mutation; a					o.				affect e.g.	jlish.	hey were created to ide they were created to ide they were created to ide they were created counciles are character compounds which ifying compounds which if creeptor binding. It receptor binding. It rangenic non-human are ocan be used as an in vivo assay ate atherosclerosis ance
		de,		\$	sho	ecel				480	6181		٠ <u>٠</u>		ich For,	Engli	ent applement applement applement applement applement can be a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article at a article article article article at a article artic
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		standard; peptide;		st entry)	peptide	oteoglycan re lipoprotein;				99WO-US004805	98US-0077618P	CALIFORNIA.	Boren JOS	و.	nds which used for,	70pp;	22-Y30700 represent apo-Bl br mutations. They were cr a theroscalerosis. The pe- of a pobBlO0. The method of neity lipoprotein (LDL) bi used for identifying comp: inhibiting LDL receptor or prevent the formation or prevent the formation sclerosis. The transgenic sclerosis. The transgenic at the person of the use that which modulate atheros
<u> </u>		ırd,		(first		log]				998	186	LI	æ	9/4	ian,	57;	re oproprior ing ing
78888888888888888888888888888888888888		nda		#	ive			•					ŢĽ,	150	COUT	Page	30700 refutcheroadly apollogy lipoping for ichibiting the properties of the properti
4 4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6		30685	AAY30685;	7-NOV-1999	Apo-B100 derived	Apo-B100; prolow density	Synthetic. Homo sapiens	WO9946598-A1	5-SEP-1999.	5-MAR-1999;	0-MAR-1998;	(REGC ) UNIV	Innerarity T	WPI; 1999-5515	Identifying compounds with proteoglycan, us atherosclerosis.	Claim 17; Pa	receptor mutation modulate atheron modulate atheron 10 a 367 of apoBlow density lip can be used for without inhibit: reduce or preverse atherosclerosis atherosclerosis express human a study of atheron compounds which
0 C C C C C C C C C C C C C C C C C C C		30E		DT 17					PD 16	PF 05	-						

N

Sequence 10 AA;

```
ö
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                             Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                       Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                            ..
                                                                                                 100.0%; Score 49; DB 2; Length 10; 100.0%; Pred. No. 0.0044; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                   AAY30686 standard, peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0077618P.
                                                                                     Query Match
Beet Local Similarity 100.0%
                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA,
                                                                                                                                            1 TRLTRTRGLK 10
                                                                                                                                                                   1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-551509/46.
                                                                           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                             Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                  17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                             W09946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1999.
                                                                                                                                                                                                                                            AAY30686;
                                                                                                                                                                                                  RESULT 2
                                                                                                                                                                                                              AAY30686
  8888888888
                                                                                                                                                                                                                                ò
                                                                                                                                                                셤
```

```
89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Beet Local Similarity 90.00,
1000 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 AA;
                                                                            AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which are receptor mutations. They were created to identify compounds which adulate atherosclerosis. The peptides are derived from amino acids 3388 compounds to a pobB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to atherosclerosis. The transgenic non-human animals and mammals which appress human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the atherosclerosis, and in vivo assay methods for identifying also be used to identify compounds which result in an increase in a therosclerotic regions. Thus the assays may be used to determine whether form atticular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
Claim 17; Page 57; 70pp; English.
```

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atheroselerosels. The peptides are derived from animo acids 3358 to 3367 of apo8100. The method comportises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent catherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulates atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether compounds wind a principle for inhibit the formation of atherosclerotic lesions. The polynucleotides can also be their animal or mammal
                                                       ö
                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                               Apo-B100; proteoglycan receptor mutation, atherosclerosis,
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                       ö
                      Length 10;
                                                      0; Indels
                    Score 45; DB 2;
Pred. No. 0.028;
                                                    1; Mismatches
                                                                                                                                                                                                AAY30684 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 57; 70pp; English.
                 91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US004805
Query Match
Best Local Similarity 90.0.
9; Conservative
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA
                                                                                  1 TRLTRTRGLK 10
                                                                                                     [|||||||||||
TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atherosclerosis.
                                                                                                                                                                                                                                                                17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                 AAY30684;
                                                                                                                                                                RESULT 3
                                                                                                                                                                                  AAY30684
                                                                                ð
                                                                                                              셤
```

ö

Gaps

ö

1; Indels

0; Mismatches

Score 44; DB 2; Length 10; Pred. No. 0.045;

ઠ

셤

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-FG binding with broteoglycan (FG). The method compounds used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the carbon compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identify compounds which result in an increase in a therosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                    Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 2;
Pred. No. 0.071;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30687 standard, peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0077618P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boren JOS;
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 rklrkekck 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Innerarity TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                      17-NOV-1999
                                                                                                                                                                                                                                                                                                      WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                       16-SEP-1999
                                                                                                                                                                                                                                       Synthetic
                          AAY30682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY30687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY30687
    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2×2×2×2×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerosals. The peptides are derived from amino acids 3358 to 3367 of apoblio. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can select to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the contact of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                               Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                   Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%; Score 43; DB 2;
90.0%; Pred. No. 0.071;
tive 0; Mismatches
                                                                                                                                        AAY30683 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0077618P
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
||||| ||||
TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1999;
                                                                                                                                                                                                                                     17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                      AAY30683;
```

ö

Gaps

.. 0

Length 10; 1; Indels

DB 2;

AAY30682 standard; peptide; 10 AA.

RESULT 5 AAY30682 ID AAY3

Best Loc Matches

8 셤 4

```
AAY30582-Y30700 represent apo-Bl00 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosels-rosals. The peptides are derived from amino acids 3158 to 3167 of apoBl00. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (FG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which atheroselerosis. The be used as an in vivo model system for the study of atheroselerosis, and in vivo assay methods for identifying compounds which modulate atheroselerosis and/or LDL-PG binding. They can atheroselerotic regions. Thus the assays may be used to determine whether a particular food or drug compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the read at the polymucleotides can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                          Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 2; Length 10;
Pred. No. 0.071;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                        98US-0077618P
                                                                                                                                                                                      99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo B binding site peptide 2.
                                                                                                                                                                                                                                                                                               Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRLTRORGIK 10
                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                                                                           WO9946598-A1
                                                                                                                                                                                                                        10-MAR-1998;
                                                                          Homo sapiens
                                                                                                                                                                                    05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9813385-A2
                                                                                                                                             16-SEP-1999
                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57205;
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BXSXEXEXEXEXEX SXE
```

```
The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide ocmponent that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with a sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Nonaturally occurring, receptor-competent LDL particles are useful as: (1) drug-teageting vectors for delivering anticancer drugs to cancer cells drugter especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                          Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 2;
Pred. No. 0.079;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                           Claim 12; Page 52; 73pp; English.
                                                                                                                                                Baillie
                                               97WO-GB002610
                                                                                96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                            (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                             Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||| || || TRLTRKRGLK 11
                                                                                                                                                                            WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                            25-SEP-1997;
                                                                              27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1997;
                 02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J2-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
AAW57207
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

96GB-00020153.

27-SEP-1996;

ó

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                        The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein ceeptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARKKWARRH (1) or TRALTKRAGIK (2), or their clamers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide fragments of apo: lipo: protein B-100 with anticoagulant activity
                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 2; Length 13;
Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FREE HOSPITAL SCHOOL MED.
                                       Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW41261 standard; peptide; 15 AA.
                                                                                                                                                   Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-GB001255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96GB-00009702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruckdorfer KR, Ettelaie C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1998 (first entry)
             (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                        Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||| ||||
TRLTRKRGLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prothrombinase complex.
                                                                   WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPI; 1998-008798/01
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9743311-A1
                                       Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW41261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        유
```

```
This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). 21-KAQ-XI-KACKREMS-XZ-T-ZZ (1) XI = S or Y; XZ = T or I; Z1 = the N terminus of the peptide, or 1-47 anino acids (as); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibite active as such or as part of a 98-aa petide, inhibite active as such or as part of a 98-aa peride, inhibite activation of the prothrombinase complex; and prevents activation of the gractor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96878-97 represent nuclear localisation signal sequence derived from
used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%; Score 43; DB 2; Length 15; 90.0%; Pred. No. 0.11; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RC, Moore JP;
                                                                             60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96892 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-00874807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guevara JG, Hoogeveen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||| ||||
TRLTRKRGLK 10
                                                                          Disclosure; Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96892
```

Ş

AAW57208 standard; peptide; 22

AAW57208

AAW57208;

TRLTRTRGLK 10 7 TRLTRKRGLK 16

н

셤 ò

9

```
ö
human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The appolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumarcid arthritis, diabetic retinopathy and hypoxia. This agguence represents a heparin binding peptide relating to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                        2; Length 15;
                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                      DB 2;
0.11;
                                                                                                                                                                                                                     Score 43; DB 2
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                     ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                  87.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-2002; 2002WO-US023419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-2001; 2001US-0306726P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retinopathy and hypoxia.
                                                                                                                                                                                                                                                                             1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                      TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ETHZ-) ETH ZUERICH (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-300420/29
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                      Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003007689-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                    ABJ37575;
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                        ABJ37575
   886666666666668888
                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                           셤
```

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density liopprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 liopphilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKNNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture medial aspecially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide binding to apo B protein delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 2; Length 22;
Pred. No. 0.16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                           Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                            note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                            /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baillie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.8%;
90.0%;
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 AA;
                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                       Modified-site
                                                                03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1996;
                                                                                                                                                                                                                                                                                                                          WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halbert GW,
                                                                                                                                                                                                                                                                                                                                                       02-APR-1998
                                                                                                                                                                                             Synthetic.
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

ö

Gaps

ö

1; Indels

87.8%; Score 43; DB 6; Length 20; 90.0%; Pred, No. 0.14;

Query Match
Best Local Similarity 90.0
Matches 9; Conservative

0; Mismatches

Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;

18-JUL-2000; 2000GB-00017641. 18-JUL-2001; 2001WO-GB003212.

WO200206314-A2 Homo sapiens

24-JAN-2002

peptide p62

(ARKT-) ARK THERAPEUTICS LTD

WPI; 2002-179777/23

Narvanen O,

Human apoB-100 derived peptide p62.

(first entry)

17-MAY-2002

AAE14541;

```
용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-atturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein ceceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARXKAGKHRH (1) or TTRLTRKRGIK (2), or their cimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives corring, receptor-competent LDL particles are corring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                       Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 22;
                                                                                                                   Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                          /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.8%; Score 43; DB 2; 90.0%; Pred. No. 0.16; tive 0; Mismatches
                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Owens MD, Baillie G;
                                             AAW57209 standard; peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                   97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                           96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that express this receptor.
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                  (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 22 AA;
                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                    WO9813385-A2
                                                                                                                                                                                                                                                                                                                   25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                           27-SEP-1996;
                                                                                            03-AUG-1998
                                                                                                                                                                                                                                                                                           02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                         Halbert GW,
                                                                                                                                                                                           Synthetic.
                                                                    AAW57209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

```
ö
New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                  The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample autoantibodies for oxLDL in a sample, especially a serum or plasma sample cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apole-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.8%; Score 43; DB 5; Length 34; 90.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96876 standard; peptide; 36 AA.
                                                                                                                                                      Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 TRLTRKRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1999
                                                                                               lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW96876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
AAW96876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

ö

Gaps ö

1; Indels

9; Conservative 1 TRLTRTRGLK 10 TRLTRKRGLK 16

Local Similarity

Best Loc Matches

8

AAE14541 standard; peptide; 34 AA.

RESULT 14 AAE14541 us-09-823-418-4.rag

```
AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major aportotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a The present sequence can be used in the composition of the invention. The present apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                            Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                               Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                          Claim 16; Fig 12C; 293pp; English
                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                              97US-00874807.
98US-00079030.
                                                                                                             98WO-US011927.
                                                                                                                                                                                                                                                             WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 AA;
               Homo sapiens
                                                                                                               10-JUN-1998;
                                                                                                                                              13-JUN-1997;
                                                                                                                                                               14-MAY-1998;
                                                WO9856938-A1
                                                                                17-DEC-1998,
                                                                                                                                                                                                                                                                                                                                treatment.
```

Search completed: December 29, 2004, 12:28:48 Job time : 61.0227 Becs

ö

0; Gaps

Query Match

87.8%; Score 43; DB 2; Length 36;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 1; Indels

1 TRLTRTRGLK 10 ||||| |||| 11 TRLTRKRGLK 20

à

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec 9

US-09-823-418-4 1 TRLTRTRGLK 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		d				SUMMAKIES	
Result	27.00	Query	V Tength	ל ב	ď	Ę	Description
			5		H		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
-	43	87.8	9 596	9	~	832802	apolipoprotein B -
7	43	87.8	4		_	LPHUB	apolipoprotein B-1
m	39	79.6			~	C60950	apolipoprotein B-1
4	39		6 77		~	JH0102	apolipoprotein B -
S	37				~	E60950	apolipoprotein B-1
9	36	73.5	5 309		~	AH0906	conserved hypothet
7	35	71.4			~	A75337	exonuclease SbcC -
80	34	69.4				E65112	hypothetical 34.6
O	34	69.4				E85985	
10	34	69				B91140	hypothetical prote
11	33					G87383	acetyltransferase,
12	33	67.3			ر.	A60950	apolipoprotein B-1
13	33	67.3			~	D70375	transcription term
14	33	67.3		О	C)	T49646	hsp70 related prot
15	33	67.3	3 78,	***	~	JH0101	apolipoprotein B-1
16	32	65.			~	G71305	probable ribosomal
17	32	65.			ς.	T16727	hypothetical prote
18	32	65.3			c)	G95913	_
19	32	65.3			_	828609	phosphoadenylyl-su
20	32	65.			~1	E83363	hypothetical prote
21	32	65.			C)	S39854	traX protein - Str
22	32	65			N	T17033	leucine rich repea
23	32	65.			N	S48288	probable phosphopr
24	32	69			~	T09313	immediate-early pr
25	32	65.			~	B87455	DNA repair protein
56	32	65			~	S40051	starch synthase (E
27	32	65.		0		G64921	probable membrane
28	32	65	3 91.	_		A39967	inter-alpha-trypsi
29	32	65	7	4		873171	DNA-directed RNA p

hypothetical prote	myc-like regulator	hypothetical prote	hypothetical prote	hypothetical prote	28.9K basic DNA-bi	DNA processing pro	probable threonin	threonine dehydrat	ubiquinol-cytochro	conserved hypothet	pyruvate dehydroge	translation initia	hypothetical prote	cobyric acid synth	ferrous iron trans
A71072	T14681	T05763	E72514	T15383	A36949	D83958	A98146	AC3142	862596	B90448	DEHUPT	822579	E83061	AD3338	875294
7	N	N	N	~	N	N	~	N	7	N	-	N	~	~	-
106	146	202	208	256	260	302	304	336	339	377	388	391	412	206	614
63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3
31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: O6-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004
C;Accession: 832802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchir Biochim. Bioc

A;Molecule type: mRNÅ \*Residues: 1-596 cAPA-A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301 C;Superfamily: apolipoprotein B

ö Gaps ö Length 596; 1; Indels Score 43; DB 2; Pred. No. 0.81; 0; Mismatches 87.8%; 90.0%; 

apolipoprotein B-100 precursor - human

N.Contrains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74 C;Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004 C;Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A2 4452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058 R;Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sc. DNA 6, 363-372, 1987

Altitle: DNA sequence of the human apolipoprotein B gene.
A; Reference number: A27850; MUID:88003974; PMID:3652907
A; Reference number: A27850; MUID:88003974; PMID:3652907
A; Rolecule type: DNA
A; Molecule type: DNA
A; Rolecules: 1-617, A', 619-1929, F', 1931-3318, D', 3320-3426, T', 3428-3431, O', 3433-3731, A; Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:O9UNNO; UNIPROT: 5, 3495-3507, 1986
B; Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
B; Ricladaras, C.; 3495-3507, 1986
A; Ricladaras, C.; Atherence and structural analysis of human apolipoprotein B-100: r. A; Reference number: A91058; MUID:87161758; PMID:3030729

A;Molecule type: mRNA A;Residues: 1-11,15-2539,'8',2541-3823,'R',3825-4563 <CLA> A;Note: 1109-Asp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

```
A; Accession: A28002
                                                                                                                                                                                                                                                                                                                                                                                       AjAccession: A23817

AjAccession: A23817

AjAccession: A23817

AjAccession: A23817

AjAccession: A23817

AjAccession: A23817

AjAccession: A23817

AjAccession: A2391 cap.

AjAccession: A2391 cap.

AjAccession: A2391 cap.

AjAccession: A2391 cap.

AjAccession: A25774

AjAccession: A25774

AjAccession: A25774

AjAccession: A25774

AjAccession: A25775

AjAccession: A25775

AjAccession: A25775

AjAccession: A25775

AjAccession: A25776

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A25777

AjAccession: A2577

                                                                                                                            A; Molecule type: mRNA
A; Residues: 485-617, 'A', 619-1044 < LA2>
A; Cross-references: GBM12480; NID:9178791; PIDN:AAAS1751.1; PID:9178792
R; Protter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr
A; Reference number: A94088; MUID:86149325; PMID:3513177
ritte: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
Reference number: A93639; MUID:87016385; PMID:3763409
```

m

```
79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||| ||||
642 SRLTRKRGLK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 TSLTRKRGLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: E60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: E60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: apoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su FrEBS Lett. 170, 105-106, 1984
A;Titcle: Human apolipoprotein B: partial amino acid sequence.
A;Tettle: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID: 84208786; PMID: 6373369
A;Accession: A22006; MUID: 84208786; PMID: 6373369
A;Accession: A22006
A;Molecule type: protein
A;Residues: 873-822. "K', 894-896 <LE1>A;Accession: B22006
A;Molecule type: protein
A;Residues: 873-822. "K', 894-896 <LE1>A;Accession: B22006
A;Molecule type: protein
A;Residues: 1313, "L', 3115-3130, "K', 3132-3133, "P', 3135-3136, "K', ALE2>
A;Accession: B22006
A;Molecule type: protein
A;Residues: 271, 12564, MUID: 87057153; PMID: 246672
A;A;Title: Structure of the human apolipoprotein B gene.
A;A;Cuntents: amordation; gene structure
B;Magener, R.; Ffitzner, R.; Stoffel, W.
B;Molecule on the organization of the human apolipoprotein B 100 gene.
A;Reference number: A92564; MUID: 87271140; PMID: 2886136
A;Contents: amordation; gene structure
A;Reference number: A92665; MUID: 87271140; PMID: 2886136
A;Reference number: A92665; MUID: 87271140; PMID: 2886136
A;Reference number: A92665; MUID: 87271140; PMID: 2886136
A;Reference number: Apgroscien B-100 heparin-binding and disulfide bond
A;Reference number: Apgroscien B-100 heparin binding md disulfide bond
A;Reference number: Apgroscien B-100 heparin binding protein.
A;Reference number: Apgroscien B is a calcium binding Protein.
A;Reference number: Apgroscien B is a calcium binding R;Carlson, P: Olosson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, G.
A;Title: Apolipoprotein B is a calcium binding R;Carlson, P: Olosson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, G.; A;Title: Mulphy: Res. I 20118; MulD: 86093680; PMID: 3841204
A;Reference number: 137189; MUID: 86093680; PMID: 3841204
A;Reference number: I 371189; MUID: 86093680; PMID: 3841204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apolyporotein B-100 - golden hamster (fragment)
C,Species: Mesocricetus auratus (golden hamster)
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C,Accession: C60950
R,Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A,Title: A cross sepecies comparison of the apolipoprotein B domain that binds to the LDL
A,Reference number: A60950; MUID: 90324804; PMID: 2373961
A,Recession: C60950
A,Molecule type: DNA
A,Residues: 11269 <LAW>A,Residues: 11269 <LAW>A,Residues: 11269 <LAW>A,Residues: 1269 <LAW>A,Residues: atheroscieros: UNIPROT: Q60536
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.8%; Score 43; DB 1; Length 4563; 90.0%; Pred. No. 5.8; ive 0; Mismatches 1; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 2
Pred. No. 2.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3385 rkirkkicik 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||| ||||
216 SRLTRKRGLK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

RESULT

```
apolipoprotein B - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Accession: JH0102
R;Smith, T.J.
submitted to GenBank, June 1990
A;Accession: JH0102
A;Accession: JH0102
A;Accession: JH0102
A;Accession: JH0102
A;Accession: JH0102
A;Accession: JH0102
A;Accession: JH0102
A;Accession: JH0102
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH0101
A;Accession: JH01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Kejwords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein, F;435-445/Region: receptor binding F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rilaw, A.; Scott, J.
Lighd Res. 31, 1109-1120, 1990
A;Titled Res. 31, 1109-1120, 1990
A;Title A cross-species comparison of the apolipoprotein B domain that binds to the LDF A;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-275 <LLAW>
A;Cross-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0906 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H.T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apolipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 2; Length 275;
Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2;
Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
```

ò 셤

ö

70.0%;

```
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: B91140
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: ECs4090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                            g
                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical 34.6 kD protein in arcB-gltB intergenic region - Escherichia coli (strain K C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Ttle: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-309 «BLAT>
A;Crose-references: UNIRROT:P45476; GB:AE000400; GB:U00096; NID:g2367203; PIDN:AAC76243.
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yhcc
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Dainococcus radiodurans
C;Species: Dainococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R;Mhite, 0.; Esisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maritle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Tetersone number: A75250; MUD:20036896; PMID:10567266
A;Accession: A7537
A;Status: preliminary
A;Accession: A7537
A;Accession: A7537
A;Accession: DNA
A;Residues: 1-909 <a href="https://www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.min.au/www.mi
Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
Reference number: AB0502; MUID:21534947; PMID:11677608
Accession: AH0906
                                                                            A;Accession: AH0906
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <PAR>
A;Cresidues: 1-309 <PAR>
A;Cresidues: GB:ALS13382; PIDN:CAD07846.1; PID:g16504394; GSPDB:GN00176
C;Genetics:
A;Gene: STX3508
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; Length 309;
Pred. No. 12;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.4%; Score 35; DB 2; Length 909; 77.8%; Pred. No. 52; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exonuclease SbcC - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 TRIARERGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:||||| |
86 RVTRTRGRK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Cross-references:
A/Experimental sour
C/Genetics:
A/Gene: DR1922
A/Map position: 1
```

d à

```
hypothetical protein yhcc [imported] - Escherichia coli (strain O157:H7, substrain EDL93. C;Species: Escherichia coli (cjate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accasion: EB5985 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P45476; GB:AE005174; NID:g12517812; PIDN:AAG58345.1; GSPDB:G.A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein EC84090 [imported] - Escherichia coli (strain O157:H7, substrain RI Cispecies: Escherichia coli (Cispecies: Escherichia coli (Cispecies: Bacherichia coli (Cispecies: Bacherichia coli (Cispecies: Bacul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 (Cispeciesion: B91140 (Cispeciesion: B91140 (Cispeciesion: B1140 (Cispeciesion: B1140 (Cispeciesion: B1120 (Cispeciesion: Cispeciesion: Cis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1.309 <HAY>
A;Cross_references: UNIPROT:P45476; GB:BA000007; PIDN:BAB37513.1; PID:g13363563; GSPDB:G
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: yhcC
C; Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acetyltransferase, GNAT family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.4%; Score 34; DB 2; Length 309; 70.0%; Pred. No. 30; 1.1ve 1; Mismatches 2; Indels
                                                          IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.4%; Score 34; DB 2; Best Local Similarity 70.0%; Pred. No. 30; Matches 7; Conservative 1; Mismatches
Pred. No. 30;
L; Mismatches
                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 70.0
                                                                                                                                                                                                                                                                   170 rolakorcik 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 TOLARQRGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 roczkokck 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRTRGLK 10
```

ö

DB 1; Length 309;

69.4%; Score 34;

Query Match

ហ

ö

Gaps ö

```
hsp70 related protein [imported] - Neurospora crassa
N;Alternate names: protein B5022.280
C;Species Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49646
S;Schulte, U.; Algin, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Law, A.; Scott, J.
T. Ligid Res. 31, 1109-1120, 1990
A;Titlaid Res. 31, 1109-1120, 1990
A;Titla A cross-species comparison of the apolipoprotein B domain that binds to the LD A;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross references: MGI:88052
C; Superfamily: apolipoprotein B
C; Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JH0101

apolipoprotein B-100 - mouse (fragment)

c)Species: Mus musculus (house mouse)

c)Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

c)Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

c)Accession: JH0101, S33128, D60950

R;Smith, T.J.; Hautama, D.; Maeda, N.
Gene 87, 309-310, 1990

A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of A;Reference number: JH0101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Crовя-references: UNIPROT:Q9P5S4; EMBL:AL355932; GSPDB:GN00116; NCSP:B5O22.280
A;Experimental source: BAC clone B5O22; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
    Length 436
                                                                                                      1; Indels
         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 2
Pred. No. 68;
3; Mismatches
         8
                                                     Pred. No. 66;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A,Residues: 1-784 <SMI>
A,Cross-references: UNIPROT: 061314; GB:M35186
R,Smith, T.; Hautamaa, D.; Maeda, N.
submitted to the EMBL Data Library, May 1989
    Score 33;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 427-531,'S',533-700 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Reference number: S33128
A,Accession: S33128
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-531, 'S',533-784 <SM2>
A,Cross-references: EMBL:X15191
67.3%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.3%;
                                                     Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 87/1; 161/2; 339/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| |:|::
404 TRLTTTKGVE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLTRTRGLK 10
                                                                                                                                                                                                  3 LTRTRGLK 10
                                                                                                                                                                                                                                                                                     LTRITGIK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-449 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: NCSP: B5022.280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T49646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                          40
         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
         Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.C.; Peldblyum, T.V.; Paulsen, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Mitle: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Accession: G871383
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-173 cSTO>
A; Cossereferences: UNIPROT:Q9A9B1; GB:AE005673; NID:g13422385; PIDN:AAK23067.1; GSPDB:GCGGenetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 poblipoprotein B-100 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus
C;Accession: A60550
B;Law, A.; Scott, J.
Lipid Res. 31, 1109-1120, 1990
A;Title: A cross species comparison of the apolipoprotein B domain that binds to the LDI
A;Reference number: A60950, MUID:90324804; PMID:2373961
A;Reference number: A60950, MUID:90324804; PMID:2373961
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues: 1-274 <LAN>
A;Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392, 353-358, 1998

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:9819666; PMID:9537320

A;Accession: D70375

A;Accession: D70375

A;Residues: DNA

A;Residues: 1-436 <AQP:
A;Acrossion: DNIPROT:067031; GB:AE000711; NID:g2983401; PIDN:AAC06989.1; PID:g298

A;Genetics:
A;Genetics:
C;Genetics:
C;Genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription termination factor Rho - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: D70375
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.3%; Score 33; DB 2; Best Local Similarity 87.5%; Pred. No. 42; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 2
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.3%;
ilarity 77.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRIMRARGL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTRKRGLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 7; Conserv
```

ઠે

ਨੇ g ö

Gaps

F;435-445/Region: receptor binding F;646-656/Region: receptor binding

0; Gaps Query Match 67.3%; Score 33; DB 2; Length 784; Best Local Similarity 70.0%; Pred. No. 1.2e+02; Matches 7; Conservative 1; Mismatches 2; Indels

0;

1 TRLTRTRGLK 10 :||||||| 647 SRLMRKRGLK 656

ò

q

Search completed: December 29, 2004, 12:39:02 Job time : 10.6591 secs

Q7zet5 human immun Q8ccc7 mus musculu Q8dwa streptococc Q6z4nl oryza sativ Q8bbi pseudomas Q7z405 homo sapien Q7th63 mus musculu Q6c4t4 yarrowia li Q9rt44 deinococcus Q7x4x giardia lam Q7x4x giardia lam Q6n488 homo sapien Cae45782 homo sapien

ALIGNMENTS

PRT;

```
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-2761261, PubMed=12878460,

Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 2525-240(2003).

EMBL; AF548396; AAP97352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein B (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUB=Liver;
TISSUB=Liver;
Pape M.E., Caelle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                                                        414
45955 MW; EEFA8492157E1BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2
Pred. No. 1.8;
0; Mismatches
       Q7ZET5
Q8CCC7
Q8CCC7
Q6Z4NU
Q6Z4N1
BAC83809
Q8B851
Q7Z405
Q7TN63
SQCC DEIRA
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
Q7RCZ
                                                                                                                                                                                                                   Apolipoprotein B 100 (Fragment).
Name=apoB-100,
Aotus vociferans (Spix's owl monkey).
                                                                                                          CAE45782
                                                                                                                                                                                            Created)
                                                                                                                                                                                          (TrEMBLrel. 25, C
(TrEMBLrel. 25, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                               87.8%;
90.0%;
 0000000000
412
115
1165
289
317
317
724
724
724
851
909
1101
                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae, Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                258 TŘLTŘKŘĠĽK 267
                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                414 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                      Lipoprotein.
NON TER
NON TER
SEQUENCE 41
                                                                                                                                                                                          01-OCT-2003 (
01-OCT-2003 (
01-OCT-2003 (
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q28473
Q28473;
                                                                                                                                                                           Q7YQR5
                                                                                                                                                                                                                                                                                                                                                                                                 Matchee
                                                                                                                                                            RESULT 1
028473
                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                        sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                glaucomys v
diceros bic
                                                                                                                                                                                                                                                                                                                                                                                                                 nyctimene a
pteropus hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Octmm7 streptomyce
Aag93596 streptomy
Q7tn65 atherurus a
                                                                                                                                                                                                                                                                                                                                                                                                                                 rousettus a
                                                                                                                                                                                                                                                                                                                                                                                                                                         chaetophrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                 agouti paca
hydrochoeru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erethizon d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mesocricetu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prochloroco
gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phalanger o
                                                                                                                                                                                                                                                                                                                                                               macaca fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mesocricetu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tachyglossu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dinomys bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ornithorhyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    salmonella
                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                       December 29, 2004, 12:13:11; Search time 58.4091 Seconds (without alignments) 98.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                         homo
                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                      Q8xfv9
Q7cpn5
Q6tmm7
       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                  1825181 seqs, 575374646 residues
                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                              Q28473
Q13788
APB HUMAN
Q72600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBXFV9
Q7CPN5
Q6TMM7
AAQ93596
Q7TN65
                                                                                                                                                                                                                                                                                                                                                                                                       Q7YR10
Q7YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                        Q7YQM7
Q7YR04
Q7YR08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q60536
Q60537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28QUTS
27TUB6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7YQN2
Q7YQM9
Q7YQN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7TN70
Q9FXM2
Q8L8T0
Q9LVA4
                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77ZZ7Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVII/C
                                                                                                                                                                                                                                            UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                      DB
                                                                                         US-09-823-418-4
49
                                                                                                         TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
178
275
387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400
               Copyright
                                                                                                                                                                                                                                                                                                                             Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                       Total number of
                                                                                                                         Scoring table:
                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                OM protein
                                                                                                          Sequence:
                                                                                                                                                   Searched:
                                                                                                                                                                                                                                             Database
                                                        Run on
                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                        Š
```

ö

Gaps

ö

PRT;

2; Length 414;

N

```
NCBI_TaxID=9606;
         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                    100
         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IUMAN

APB HUMAN STANGEL.

P04114; O00502; Q13787;

01-NOV-1986 (Rel. 03, Created)

01-NOV-1986 (Rel. 03, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

05-JUL-2004 (Rel. 44, Last annotation update)

`-~~retein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-87191999; PubMed=2883086;
Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure of the B-74 region.";
Gene 49:29-51(1986).
EMBL; M15421; AAA51758.1; -.
PIR; A27850; LPHUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiena (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                         ;
0
metabolism in the cynomolgus monkey: evidence for post-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 3262;
                                                                                                                                                                                                                                                                      Length 596;
                                                                                                                                                                                                                                                                                                       Indels
                                                                                    TISSUE=Liver,
Murray R.,
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56603BC0618DD40D CRC64;
                                                                                                                                                                                                                               66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005576; C:extracellular; NAS.
GO:0005319; F:lipid transporter activity; NAS.
GO:0006869; P:lipid transport; NAS.
TER
                                                                                                                                                                                                                                                                  Score 43; DB 2;
Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 3262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 2
Pred. No. 18;
0; Mismatches
                    transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3262 AA; 370140 MW;
                                                                                                                                                                                                                                                                  87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24, APOB protein (Fragment)
                                                                                                                                        EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2084 TRLTRKKGLK 2093
                                                                                                                                                                                                                                                                                                                                                                      226 TRLTRKRGLK 235
                                                                                                                                                                                                                                                                                                                                    1 TRLTRTRGLK 10
                                                                                                                                                                                                                296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRTRGLK 10
                                                                                                                                                                                                                                 596 AA;
                                                                                                                                                                                                                                                                                 Local Similarity
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCBI_TaxID=9606;
                                                                                                                                                                                              1
596
                                                                                                                                                                         Lipoprotein.
NON TER
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q13788
Q13788;
                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
APB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
 ð
                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOOCTOOLS BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCOUNT BY ACCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OS GE DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
SEQUENCE FROM N.A.
MEDIJINE=87016385; PubMed=3763409;
KRDOLT C.C., Wallis S.C. Fowell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.C., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete CDNA and derived protein sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=8500528; PubMed=2994225; MEDLINE=8500528; PubMed=2994225; Knott T.J., Jacobson S.F., Urdea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M., Prietlelley L.M., Robertson B., Rall L.B., Betsholtz C., Shows T.B., Mahley R.W., Scott J.; "Human apolipoprotein B. structure of carboxyl-terminal domains, sites of gene expression, and chromosomal localization."; science 230:37-43(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (3) SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE=87008488; PubMed=3759943;
Ghen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
"The complete CDNA and amino acid sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 3056-3159 FROM N.A.
MEDLINE=86041888; PubMed=3903660;
Mehrablan M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgesner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [8]
SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86093680; PubMed=3841204;
Carlsson P., Olofeson S.O., Bondjers G., Darnfors C., Wiklund O.,
Bjursell G.;
                                                                                                                                                                                                                                                                                                                                                                                   SEĞUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE-88003974; PubMed-3652907;
Ludwig B.H., Blackhart B.D., Pierotti V.R., Calati L., Fortier C
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
DNA 6:363-372(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILTB=87161758; PubMed=3030729;
Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
Zannis V.I.;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of human apolipoprotein B cDNA.";
Nucleic Acids Res. 13:8813-8826(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 709-906 FROM N.A.
MEDLINE=65270450; PubMed=3860836;
Deeb S.S., Motulaky A.G., Albers J.J.;
"A partial TonA clone for human apolipoprotein B.
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 14:7501-7503(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 13:6937-6953(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 261:12918-12921(1986)
```

```
VARIANT LEU-2739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7Z600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
            MEDLINE-86149325; PubMed=3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L., "Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.";
Nature 323:738-742(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100.";
Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         당
                                                                                                                                                                                                                               PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
MEDLINE=88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cia S.-J., Deslypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.;
"Apolipoprotein B-48 is the product of a messenger RNA with an organ-
                                                                                                                                                                                                                                                                                                                                                                             MEDILINE 97039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
Levy-Wilson B., Scott J.;
"Complete protein sequence and identification of structural domains of Numan apolipoprotein B.";
Nature 323:734-738(1986).
                                                                                                             SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE=86287319; PubMed=3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M. Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of CDNA clones encoding the entire B-26 region of human apolipoprotein B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.; "Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene."; Hum. Genet. 86:91-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT FDB GLN-3527.
MEDLINE-89098975; PubMed-2563166;
Soria L.F., Ludwig B.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALMITOYLATION OF CYS-1112.
MEDLINE=20143590; PubMed=10679026;
Shao Y., McCabe J.B., Vance J., Berthiaume L.G.;
"Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprotein B ia calcium binding protein.";
Biochem. Biophys. Res. Commun. 137:493-499(1986).
                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
                                                                      apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Cell 11:721-734 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91071750; PubMed=1979313;
                                                                                                                                                                                                                                                                                                                         in-frame stop codon.";
                                                                                                                                                                                                                                                                                                                                       Science 238:363-366(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALCIUM-BINDING DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT SER-4338.
                                                                                                                                                                                                                                                                                                                                                                     DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAINS
```

```
Rabes J.P., Varret M., Saint-Joré B., Erlich D., Jondeau G.,
Krempf M., Girandet P., Junien C., Bollau C.,
"Familial ligand-defective apolipoprotein B-100: simultaneous
detection of the ARG3500--SGLN and ARG3531-->CYS mutations in a French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-10 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
                                                                                                                                                          MEDIINE=95190020; PubMed=7883971; Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.; Mendel C.M., Frost Petro, expolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                 VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
                                                                                                                                                                                                                                                                                                                                                                                                                                             Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
MEDLINE-91016974; PubMed-2216805;
Hang L.-S., Gavish D., Breslow J.L.;
"Sequence polymorphism in the mann apoB gene at position 8344.";
Nucleic Acids Res. 18:5922-5922(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND ILE-1921.
MEDIATE-9911125; PubMed-9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nickerson D.A.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 1
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ag(X) antigen).
                                                                                                                                                                                                                                                                                                          Clin. Invest. 95:1225-1234(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS FDB GLN-3527 AND CYS-3558.
MEDLINE=97403938; PubMed=9259199;
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97044521; PubMed=8889592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum. Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hum. Mutat. 8:282-285(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein B (Including Name=APOB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypocholesterolemia.";
Hum. Genet. 102:44-49(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRTRGLK 10
                                                                                                                                      VARIANT FDB CYS-3558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             population.
```

```
28:225-240(2003)
                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                        Apolipoprotein B 100 (Fragment).
                                                                                          79.6%;
          Mol. Phylogenet. Evol. 28:22
EMBL; AY243375; AAP50763.1;
                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                               8; Conservative
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                        275 SRLTRKRGLK 284
                                                                                                                                   1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :[||| ||||
279 SRLTRKRGLK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pteropodinae, Pteropus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
436 4
436 AA;
                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9405;
                                 Lipoprotein.
NON TER
NON TER
SEQUENCE 432
                                                                                                                                                                                                                                                                                 Name=apoB-100
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein.
NON TER 43
SEQUENCE 436
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                Q7YQM8
Q7YQM8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7YQM7
Q7YQM7;
                                                                                                              Matches
                                                                                                                                                                                          RESULT 8
Q7YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7YQM7
           STTWRE
                                                                                                                                    8
                                                                                                                                                        g
                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
4polipoprotein B (Fragment)
Glaucomys volans (Southern flying squirrel).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.

MEDLINES-2761261, PubMed=12878460;

Amrino-Madeen H., KoopEli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AY243379; AAP50767.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINBE-22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Am new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Rhinocerotidae, Diceros.
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.6%; Score 39; DB 2; Length 421; 80.0%; Pred. No. 13; 1.1ve 1; Mismatches 1; Indels
                                                                                                     4563 AA; S15553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 421
421 AA; 46747 MW; D47B77BD4F864FD1 CRC64;
EMBL; AY324608; AAP72970.1; -. GO; GO:0005319; F:lipid transporter activity; IEA. GO; GO:0006869; P:lipid transport; IEA. InterPro; IPR009454; DURIO81.
InterPro; IPR001747; Lipid_transport_N. Pfam; PF06448; DUF1081; 1. SMART; SM0638; LPD_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTYRIO, 01-OCT-2003 (TrEMBLrel. 25, Created) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Apolipoprotein B (Fragment).
Diceros bicornis (Black rhinoceros).
                                                                                                                                                                                                                                                        421 AA
                                                                                                                              Score 43; DB
Pred. No. 26;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 AA
                                                                                                                                                                                                                                                       PRT;
                                                                                                                             87.8%;
90.0%;
                                                                                                                                                    9; Conservative
                                                                                                                                                                                        3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRTRGLK 10
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=64683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=9805
                                                                                           Lipoprotein.
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                       Glaucomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                    Q7TN68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7YR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07YR10
   SEARCH
                                                                                                                                                                        ò
                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                             ઠે
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nyctimene albiventer (Common tube-nosed fruit bat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae;
Pteropodinae, Nyctimene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pteropus hypomelanus (Small flying fox).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                           Score 39; DB 2; Length 432;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%; Score 39; DB 2; Length 436; 80.0%; Pred. No. 14; 11; Indels 1; Indels
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
432 432
432 AA; 48171 MW; F27B7AB39604732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48717 MW; 1C4A7EAD72D2C629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-2003 (TrEMBLrel. 25, Created)
01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
10-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
Name=apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 AA.
                                                                                                                                                    1; Mismatches
```

Gaps

S F T S

ઠે g

```
MEDLINE=22761261; PubMed=12878460;
Amrine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships ";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22761261; PubMed=12878460;
Marine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; MY2431369; AAPS0757-1; ...
InterPro: IPR000871; Beta lactanase A.
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                  Agouti paca (Paca).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
NCBI_TaxID=108852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.6%; Score 39; DB 2; Length 445; 80.0%; Pred. No. 14; tive 1; Mismatches 1; Indels
                                  79.6%; Score 39; DB 2; Length 445; ilarity 80.0%; Pred. No. 14; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
 445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Fragment)
Hydrochoerus hydrochaeris (Capybara) (Carpincho)
                                                                                                                                                                                                                                                        01-077-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 AA
                                                                                                                                                                                                                               445 AA
                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 80.0
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                        288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 SRLTRKRGLK 297
                                                                                                        1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRTRGLK 10
                Query Match
Best Local Similarity
''. 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10149;
                                                                                                                                                                                                                                                                                                                                  Name=apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein.
NON TER
NON TER 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein.
NON TER
NON TER 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrochaeris
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                           Q7TN64
Q7TN64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17NT7
                                                                                                                                       g
                                                                                                          δ
                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein B (Fragment).

Rousettus amplexicaudatus (Common rousette).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammailai, Butheria; Chiroptera; Megachiroptera; Pteropodinae; Rousettus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling
wol'ence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-2761261, bubMed=12878460,

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

MOI. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243378; AAP50766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaetophractus villosus (South American armadillo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Edentata, Dasypodidae, Chaetophractus.
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.6%; Score 39; DB 2; Length 438; 80.0%; Pred. No. 14; tive 1; Mismatches 1; Indels
                                                                                                      Length 438;
                                                                                                                                        1; Indels
                                                                    48734 MW; 2BD85BCBF4E2CC41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48597 MW; 41C890DEAF95C872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment)
                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                   Score 39; DB 2;
Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                 438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 AA.
                                                                                                      79.6%;
 EMBL; AF548436; AAP97392.1;
                                                                                  Query Match
Best Local Similarity 80...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
438 AA; 48E~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                             :|||| ||||
281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||| ||||
281 SRLTRKRGLK 290
                                    1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1445
                                                                                                                                                                           1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRTRGLK 10
                                                                    438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein.
NON_TER
NON_TER 44
                  Lipoprotein.
NON_TER
NON_TER 4
SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                Q7YR04
                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
```

ð

ö

Gaps

```
à
                                                                                                                                                            셤
                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90236327; PubMed=2332175;
MEDLINE=90236327; PubMed=2332175;
MEDLINE=90236327; PubMed=2332175;
Maeda N.;
"Sequence of the putative low-density lipoprotein receptor-binding regions of apolipoprotein B in mouse and hamster.";
EMBL, M35187; AAA37059.1; -.
PIR; C60950; C60950.
                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragman annotation update)
Exethizon dorsatum (North American porcupine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammaila, Eutheria, Rodentia, Hystricognathi, Erethizontidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    060536;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Hamster apolipoprotein (apoB) (Fragment).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
               Score 39; DB 2; Length 445; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Pest Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 1; Indels
                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipoprotein.
1 1
NON_TER 445
SEQÜENCE 445 AA; 49617 MW; 9572FESF5E7625F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780 780
780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
                                                                                                                                                                                                                                                                                                                                  445 AA
                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                               PRT;
         79.6%;
                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                      :|||| ||||
288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                  1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRTRGLK 10
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=34844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein.
NON TER
NON TER 78
SEQUENCE 78(
                                                                                                                                                                                                                                                                                                                         Q7TN72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 060536
                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

0536

                                                                                                                     ò
                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

ore committee of the co

Search completed: December 29, 2004, 12:37:31 Job time : 59.5202 secs

```
December 29, 2004, 12:10:41; Search time 61.027 Seconds (without alignments) 58.786 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          2002273 seqs, 358729299 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_23Sep04:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          geneseqp1980s:*
geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  geneseqp2000s:*
geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
                                                                                                                                                                                      US-09-823-418-5
48
                                                                                                                                                                                                                          1 TRLTRSRGLK 10
                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB		escription
	48	100.0	10	7	AAY30686	Aay30686 Apo-B100
7	45	93.8	10	~	AAY30684	
m	45	93.8	10	~	AAY30685	
4	44	91.7	10	~	AAY30683	
S	44	91.7	10	~	AAY30682	
9	44	91.7	10	~	AAY30687	
7	44	91.7	11	~	AAW57205	
80	44	91.7	13	7	AAW57207	æ
σ	44	91.7	15	~	AAW41261	Aaw41261 Apolipopr
10	44	91.7	15	~	AAW96892	
11	44	91.7	20	9	ABJ37575	Abj37575 Heparin b
12	44	91.7	22	~	AAW57208	
13	44	91.7	22	~	AAW57209	Aaw57209 Apo B 100
14	44	91.7	34	ഗ	AAE14541	Aae14541 Human apo
15	44	91.7	36	~	AAW96876	Aaw96876 Nucleic a
16	44	91.7	37	~	AAW64587	Aaw64587 Human apo
17	44	91.7	51	~	AAW96845	Nuclei
18	44	91.7	343	4	ABB37687	Abb37687 Peptide #
19	44	91.7	343	4	ABG52504	Abg52504 Human liv
20	44	91.7	377	~	AAR72704	Aar72704 Human apo
21	44	91.7	377	~	AAR34031	Aar34031 Sequence
22	44	91.7	2463	æ	ADJ57400	Adj57400 Human apo
23	44	91.7	3923	~	AAY31237	Human
24	44	91.7	4536	~	AAW41262	Aaw41262 Apolipopr
	44	91.7	4536	0	AAW96826	Aaw96826 Amino aci

Aau98981 Human apo Add48677 Human Pro Aao15893 Human apo Abr40253 Human ali Abu79140 Apolipopr Add14870 Human apo Adh18870 Human apo Ado33445 Human apo Ado33447 Human apo Ado33447 Human apo Ado33447 Human apo Ado33469 Apo-B100 Aay30692 Apo-B100 Aay30692 Apo-B100 Aay30698 Apo-B100 Aay30698 Apo-B100 Aaw57206 Apo B 100 Aaw67717 Analogue Aaw67717 Analogue Aaw61732 BSWR effe Ad56451 Human apo	Aaw41260 Apolipopr
AAU98981 ADD48677 AAD15893 ABR40253 ABR40253 ABR4029140 ADH18871 ADH18870 ADH18870 ADH18870 ADH3870 AAV30690	AAW41260
0.1222222222222222222222222222222222222	7
44444444444444444444444444444444444444	-
99117777777777777777777777777777777777	81.2
4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6	39
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	45

### ALIGNMENTS

RESULT 1

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation, atherosclerosis, low density lipoprotein; proteoglycan, LDL, atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. AAY30686 standard; peptide; 10 AA. Claim 17; Page 57; 70pp; English. 99WO-US004805. 98US-0077618P. Innerarity TL, Boren JOS; (first entry) (REGC ) UNIV CALIFORNIA. WPI; 1999-551509/46. Synthetic. Homo sapiens. W09946598-A1 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999. AAY30686; AAY30686 

~

ö

Gaps

ö

Length 10; 0, Indels

Score 45; DB 2; Pred. No. 0.029; 1; Mismatches

93.8%;

2

1 TRLTRSRGLK

|||||:||| 1 TRLTRARGLK 10

셤

ð

Query Match
Best Local Similarity 90.0
Matches 9; Conservative

Sequence 10 AA;

g

```
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                ö
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                       Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                               ö
                                                                                                     100.0%; Score 48; DB 2; Length 10; 100.0%; Pred. No. 0.0073; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                            AAY30684 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0077618P
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innerarity TL, Boren JOS;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                 1 TRLTRSRGLK 10
                                                                                                                                                                        TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-551509/46.
                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis.
                                                                               Sequence 10 AA;
                                                                                                                                                                                                                                                                          17-NOV-1999
                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                   AAY30684;
                                                                                                                          Matches
  88888888
                                                                                                                                                                     셤
                                                                                                                                                                                                                            ò
```

Apo-B100; proteoglycan receptor mutation, atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation.

Homo sapiens. WO9946598-A1

Synthetic

99WO-US004805,

05-MAR-1999; 10-MAR-1998;

16-SEP-1999,

Innerarity TL, Boren JOS;

WPI; 1999-551509/46.

(REGC ) UNIV CALIFORNIA.

AAY30685 standard; peptide; 10 AA.

RESULT 3

(first entry)

17-NOV-1999

AAY30685;

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which aredeptor mutations. They were created to identify compounds which modulate atheroselerosals. The peptides are derived from anino acids 3358 to 3367 of apoB100. The method comportises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-RG binding without inhibiting LDL receptor binding. Such compounds can be used to atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the compounds which modulate atheroselerosis and/or LDL-RG binding. They can also be used to identify compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether a particular food or atury composition tends to stimulate or inhibit the formation of atheroselerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10 AA;
```

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which method receptor method compiles are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (Ed). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transpapents non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which medulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in also be used to determine whether a particular food or drug composition tends to stimulate or inhibit the correction of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.

Claim 17; Page 57; 70pp; English.

셤

```
Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                         Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                    17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                 Innerarity TL,
                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                  WO9946598-A1
                                                                                                                                                                                                                                                                                                       05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                          10-MAR-1998;
                                                                                                                                                                                                                                                                     16-SEP-1999
                                                                                                                                                                              Synthetic
                    AAY30682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY30582-Y30700 represent apo-Blo0 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apoBlo0. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and manmals which atherosclerosis, and in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                 Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                              Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 2; Length 10;
Pred. No. 0.047;
0; Mismatches 1; Indels
                                                                                                      AAY30683 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0077618P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boren JOS;
                                                                                                                                                                            17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
|||||:||||
TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Innerarity TL,
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-1999
                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                           AAY30683;
```

98US-0077618P. 99WO-US004805

Boren JOS;

```
to 3367 of appBlOG. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the strucky of atherosclerosis, and in vivo assay methods for identifying compounds which medulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the commation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                             AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358
Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; Score 44; DB 2; Length 10; 90.0%; Pred. No. 0.047; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY30687 standard; peptide; 10 AA.
                                                                                                                                                     Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTRERGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY30687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY30687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXXXXX
```

AAY30682 standard; peptide; 10 AA.

RESULT 5 AAY30682 ID AAY3

1 TRLTRSRGLK 10 TRLTRDRGLK 10

g ò

Baillie G;

```
The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media sepecially as growth supplements. Non-naturally occurring, ceceptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                 Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 52; 73pp; English.
                                                                                                                  97WO-GB002610
                                                                                                                                                                        96GB-00020153
                                                                                                                                                                                                                                     (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                              Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-230637/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||
TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11 AA;
                                                                                                            25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-Bite
                                                                                                                                                                        27-SEP-1996;
                                                      02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57207
                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transpenic non-human animals and mammals which etudy of atheroselerosis, and in vivo assay methods for identifying compounds which medulate atheroselerosis and/or LDL-PG binding. They can study of atheroselerosis, and in vivo assay methods for identifying compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.7%; Score 44; DB 2; Length 10; 90.0%; Pred. No. 0.047; 1; Indels :ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57205
ID AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                              99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                       98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo B binding site peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.00,
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRLTRORGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    10-MAR-1998;
                                                                                                                                                                                  WO9946598-A1
                                                                                                                                                                                                                                                                                                           05-MAR-1999;
                                                                                                                                                                                                                                              16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1998
                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW57205;
```

```
ö
                                                                                                                                                                                      Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDb; receptor component; apo B100 receptor site.
                       Gaps
                       ;
0
   Length 11;
                     1; Indels
                                                                                                                                                                   Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                       /note= "attached to retinoic acid"
 Score 44; DB 2;
Pred. No. 0.052;
0; Mismatches 1
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                         AAW57207 standard; peptide; 13 AA.
91.7%;
                                                                                                                                                                                                                                                                                                                                                    96GB-00020153.
                                                                                                                                                                                                                                                                                                                                  97WO-GB002610.
                                                                                                                                                 (first entry)
                    9; Conservative
                                                                                                                                                                                                                                                                                                                                25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                   27-SEP-1996;
                                                                                                                                                                                                                                                                                                              02-APR-1998
```

WO9813385-A2

Synthetic.

RESULT 7

ò a

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences. KARYKKNKHRH (1) or TRALYRKNGHK (2), or their climers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding effinity to an apo B protein receptor
                                                                                                                 Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-coagulant, apolipoprotein B-100, apoB-100, metastatic spread, thromboplastin-mediated process, cancer; inhibitor; blood coagulation, angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 13;
Pred. No. 0.062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FREE HOSPITAL SCHOOL MED.
                                                 Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                 Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96GB-00009702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-GB001255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bruckdorfer KR, Ettelaie C;
                                                                                                                                                      that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-1998 (first entry)
               (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                 Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRLTRKRGLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prothrombinase complex
                                                                                 WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPI; 1998-008798/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNLO ) ROYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9743311-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-1997;
                                               Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW4126:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
8
```

Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity

ö

Gaps

```
This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-cosqulant properties of apolioporcein B-100 (apoB-100). 21-KAQ-XX-KKWKHKHS-X2-T-Z2 (1) XI = S or Y; XZ = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (aa); Z2 = the C terminus of the peptide, or 1-47 amino acids or Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits cativation of the prothrombinase complex; and prevents activation of the prothrombinase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW96878-97 represent nuclear localisation signal sequence derived from
used for treating or preventing coagulation, inhibiting angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%; Score 44; DB 2; Length 15; 90.0%; Pred. No. 0.071; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RC, Moore JP;
                  cell differentiation and apoptosis.
                                                        60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW96892 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-00874807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guevara JG, Hoogeveen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||| |||
TRLTRKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRSRGLK 10
                                                        Disclosure; Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9856938-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW96892
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

9

```
ò
human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein (IDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                Score 44; DB 2; Length 15; Pred. No. 0.071;
                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 2; 79pp; English.
                                                                                                                                                                            fibrosis and arteriosclerosis
                                                                                                                                                                                                                                               91.7%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-2002; 2002WO-US023419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-2001; 2001US-0306726P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                        ||||| ||||
TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                                 1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETH ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-300420/29.
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003007689-A2.
                                                                                                                                                                                                              Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hubbell JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJ37575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ETHZ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYZU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    888888888888888
                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                 셤
```

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotean (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                     Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                       Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                     'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                       /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 2;
Pred. No. 0.11;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                           AAW57208 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%;
90.0%;
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRLTRKRGLK 16
                            TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1998,
                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                            AAW57208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Si
Matches 9;
                                                                             RESULT 12
                                                                                            AAW57208
                                                                                                                            셤
 ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

ô

ô

Gaps

ö

91.7%; Score 44; DB 6; Length 20; larity 90.0%; Pred. No. 0.096; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 9; Conserv

(first entry)

```
New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to peptides having affinity for oxidised low density lipoprotein (OxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                         Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-179777/23
                                                                                                                                                                                                                                                                                                                     WO200206314-A2.
                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                       peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Narvanen O,
                                              17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002
AAE14541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-caturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein creceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKKNKHH (1) or TTRLFKRRGK (2), or their claimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                        Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 2; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "attached to retinoic acid"
                                                                                                                                                                                                                                         Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Owens MD, Baillie G;
                                                                                             AAW57209 standard; peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        that express this receptor.
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-230637/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9813385-A2
                                                                                                                                                                                           03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                         AAW57209;
                                              RESULT 13
                                                                      AAW57209
```

Yla-Herttuala S

```
ö
                                                                                                                                                                                                                                                                                                                Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                          Gaps
                                                          ö
                                                                                                                                                                                                                                                                                    Nucleic acid binding domain from apoB-100, residues 3348-3390.
                         Score 44; DB 5; Length 34; Pred. No. 0.17;
                                                        1; Indels
                                                          0; Mismatches
                                                                                                                                                                                              AAW96876 standard; peptide; 36 AA.
                         91.7%;
                                                                                                                                                                                                                                                        22-APR-1999 (first entry)
                                        Local Similarity 90.0
hes 9; Conservative
                                                                                      1 TRLTRSRGLK 10
                                                                                                                  34
                                                                                                             25 TRLTRKRGLK
Sequence 34 AA;
                                                                                                                                                                                                                           AAW96876;
                             Query Match
```

0;

Gaps

ö

1; Indels

9; Conservative 1 TRLTRSRGLK 10

16

TRLTRKRGLK

ઠ 셤 AAE14541 standard; peptide; 34 AA.

RESULT 14 AAE14541 ID AAE1 XX

Homo sapiens

WO9856938-A1 17-DEC-1998.

97US-00874807. 98US-00079030. 98WO-US011927.

10-JUN-1998; 13-JUN-1997; 14-MAY-1998;

```
AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major aportotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein (VLDL). Intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The present specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                   Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                             Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Fig 12C; 293pp; English
                                                                                                                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                        treatment.
```

11 TRLTRKRGLK 20 셤

1 TRLTRSRGLK 10

ઠે

ö

Gaps ö

Query Match
91.7%; Score 44; DB 2; Length 36;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels

Search completed: December 29, 2004, 12:28:48 Job time : 61.0227 secs

Sequence 14, Appl Sequence 4, Appl Sequence 4, Appli Sequence 2245, A Sequence 30, Appl Sequence 361, Appl Sequence 51, Appl Sequence 1915, Appl Sequence 2288, Appl Sequence 281, Appl Sequence 6931, Appl Sequence 6931, Appl Sequence 2841, Appl Sequence 77577, Appl Sequence 77577, Appl

ALIGNMENTS

Sequence Seq

```
APPLICATE AGNELLO, VINCENT
TITLE OF INVENTION: METHOD OF INHIBITING INFECTION BY HCV, OTHER
TITLE OF INVENTION: PLAVIVIRIDAE VIRUSES, AND ANY OTHER VIRUS THAT
TITLE OF INVENTION: COMPLEXES TO LOW DENSITY LIPOPROTEIN OR TO VERY LOW
TITLE OF INVENTION: DENSITY LIPOPRIODIN IN BLOOD BY PREVENTING VIRAL ENTRY
TITLE OF INVENTION: INTO A CELL
FILE REPERENCE: 1513-PCT-0
CURRENT APPLICATION NUMBER: US/10/398,200
CURRENT APPLICATION NUMBER: 60/243,594
PRIOR PELING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 6; Length 4560;
Pred. No. 3;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alitalo et al.
TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
FILE REFERENCE: 28967/393594
CURRENT APPLICATION NUMBER: US/10/868,577A
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US 60/478,390
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-09-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
            US-10-511-989-14
US-10-511-989-14
US-10-511-989-12
US-10-983-340-4
US-10-220-366A-22245
US-10-929-30
US-10-929-30
US-10-408-765-80
US-10-408-765-1915
US-10-408-765-1915
US-10-408-765-1915
US-10-408-765-1915
US-10-408-765-1915
US-10-408-765-1915
US-10-408-765-1915
US-10-408-765-1917
US-10-408-765-2841
US-10-408-765-2841
US-10-408-765-2841
US-10-408-765-2841
US-10-408-765-2841
US-10-408-765-2841
US-10-408-765-2841
PCT-US02-09107B-66243
                                                                                                                                                                                                                                                                                                                               US-10-732-923-9577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-868-577A-25; Sequence 25, Application US/10868577A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/10398200 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.7%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.vv,
P. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver. 2.1
3382 TRLTRKRGLK 3391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
LENGTH: 4560
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-398-200-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-398-200-2
 SEQ ID NO 2
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Appli
Sequence 25, Appl
Sequence 72046, A
Sequence 5628, Ap
Sequence 5939, Ap
Sequence 576, Appl
Sequence 70, Appl
Sequence 8115, Ap
Sequence 8115, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74744, p. Sequence 51874, p. Sequence 42481, p. Sequence 42504, p. Sequence 72504, p. Sequence 11685, p. Sequence 11685, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 11687, p. Sequence 116887, p. Sequence 11687, p. Sequence 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69335,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                              December 29, 2004, 12:28:58 ; Search time 8.97727 Seconds (without alignments) 51.960 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1
Sequence 6
Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-868-577A-25
US-11-001-793-5028
US-11-001-793-5028
US-11-001-793-5039
US-10-482-526A-576
US-10-990-328-8115
US-10-990-328-8115
US-10-990-328-8115
US-10-990-328-8116
US-10-990-328-8116
US-10-990-328-8116
US-10-990-328-8116
US-10-990-328-8116
US-10-990-328-8116
US-10-990-328-8116
US-10-990-328-8116
US-10-990-91078-738-8
PCT-USOZ-091078-7444
PCT-USOZ-091078-7444
PCT-USOZ-091078-738-8
PCT-USOZ-091078-738-8
PCT-USOZ-091078-72662
PCT-USOZ-091078-72662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-990-328-13596
US-10-990-328-11685
US-10-990-328-11686
US-10-990-328-11687
US-10-990-328-11689
                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             187395 segs, 46645940 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                       US-09-823-418-5
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                                                                                                                                                                        1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
```

ö

Gaps

```
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR PELING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,845
PRIOR PLILING DATE: 1997-06-22
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-05-23
PRIOR PLLING DATE: 1997-05-23
PRIOR PLLING DATE: 1997-06-23
PRIOR PLLING DATE: 1997-08-2
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-05-23
PRIOR PLLING DATE: 1997-06-23
PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PLING PRIOR PRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.8%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-001-793-5628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ORGANISM: Homo sapiens
US-11-001-793-5939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 TRLRRSRG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRSRG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Eliters Pharmaceuticals Inc.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT APPLICATION NUMBER: PCT/USO2/09107B
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2001-09-05
PRIOR PAPLICATION NUMBER: 09/948,993
PRIOR PAPLICATION NUMBER: 00/342,923
PRIOR PILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 78614
SCPT THE OF SEQ ID NOS: 78614
CFD THE OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%; Score 44; DB 6; Length 4563; 90.0%; Pred. No. 3; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.2%; Score 38; DB 1; Length 289; Best Local Similarity 88.9%; Pred. No. 2.8; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5628. Application US/11001793
Sequence 5628. Application US/11001793
GENERAL INFORMATION:
APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS90
CURRENT APPLICATION NUMBER: US/11/001,793
CURRENT FILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: US/10/100,683
PRIOR FILING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (32) ... (126)
OTHER INFORMATION: heparin binding domain
FEATURE:
                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

// LOCATION: (3161)..(3236)

// OTHER INFORMATION: heparin binding domain

US-10-868-577A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 72046, Application PC/TUS0209107B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Streptococcus mutans
PCT-US02-09107B-72046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 RLVRSRGLK 249
                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 RLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -US02-09107B-72046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 72046
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

| Sequence 5939, Application US/11001793
| GENERAL INFORMATION:
| APPLICANT: Rosen, et al.
| TITLE OF INVENTION: Human Secreted Proteins
| FILE REFERENCE: PS900
| FILE OF INVENTION: Human Secreted Proteins
| FILE REFERENCE: PS900
| FILE REFERENCE: PS900
| FILE REFERENCE: PS900
| FILE REFERENCE: PS900
| FRICK APPLICATION NUMBER: US/10/100,683
| FRICK APPLICATION NUMBER: US 60/040,162
| FRICK APPLICATION NUMBER: US 60/040,162
| FRICK APPLICATION NUMBER: US 60/043,576
| FRICK APPLICATION NUMBER: US 60/043,500
| FRICK APPLICATION NUMBER: US 60/043,580
| FRICK APPLICATION NUMBER: US 60/043,580
| FRICK APPLICATION NUMBER: US 60/043,580
| FRICK APPLICATION NUMBER: US 60/043,380
| FRICK APPLICATION NUMBER: US 60/043,380
| FRICK APPLICATION NUMBER: US 60/043,314
| FRICK APPLICATION NUMBER: US 60/043,314
| FRICK APPLICATION NUMBER: US 60/043,314
| FRICK APPLICATION NUMBER: US 60/043,314
| FRICK APPLICATION NUMBER: US 60/043,314
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
| FRICK FILING DATE: 1997-04-13
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 7; Length 470;
Pred. No. 48;
0; Mismatches 1; Indels
Score 33; DB 7; Length 62;
Pred. No. 5.9;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 68.8%;
Best Local Similarity 87.5%;
Matches 7; Conservative
```

```
TITLE OF INVENTION: Methods and Compositions for the Introduction of Polynucleotides FILE REFERENCE: 120701-2030
CURRENT APPLICATION NUMBER: 2004-10-25
PRIOR APPLICATION NUMBER: 60/568,436
PRIOR FILING DATE: 2004-6-05
PRIOR FILING DATE: 2004-0-24
NUMBER OF SEQ ID NOS: 218
SOFTWARE: Patentin version 3.3
SOFTWARE: 984 DIOR 10-24
NUMBER OF SEQ ID NOS: 218
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLBIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CL001495
CURRENT APPLICATION NUMBER: US/10/990,328
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558824
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8115
LENGTH: 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10

US-10-990-328-8116

S. SQUADORO E 8116, Application US/10990328

S. SQUADORO E 8116, Michele

TITLE OF INVENTION: BOLYMORPHISMS IN NUCLEIC ACID MOLECULES

TITLE OF INVENTION: BACODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/10/990,328

CURRENT APPLICATION NUMBER: US/10/990,328

CURRENT PILING DATE: 2004-11-17

NUMBER OF SEQ ID NOS: 558824

S. SOFTWARE: PRECED FOR WINGOWS VERSION 4.0

SEQ ID NO 8116

LENGTH: 441
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 6; Length 388;
Pred. No. 63;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%; Score 32; DB 6; 70.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 8115, Application US/10990328 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     66.7%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 rvirkaegik 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 TVLTRAEGLK 61
                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-10-972-963-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Homo sapiens
US-10-990-328-8115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-990-328-8116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-10-990-328-8115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70, Application PC/TUS0435137
GENERAL INFORMATION:
APPLICANT: Gencia Corporation
APPLICANT: Gencia Corporation
APPLICANT: Khan, Shaharyar
TITILE OF INVENTION: Methods and Compositions for the Introduction of Polynucleotides
FILE REFERENCE: 120701-2030
CURRENT APPLICATION NUMBER: PCT/US04/35137
CURRENT APPLICATION NUMBER: 60/568,436
PRIOR APPLICATION NUMBER: 60/568,436
PRIOR PRILING DATE: 2004-05-05
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 218
NUMBER OF SEQ ID NOS: 218
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%; Score 32; DB 6; Length 309; 77.8%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 388;
                                                                                                                                                                                  APPLICATION PARTICIPATIONS AG
TITLE OF INVENTION: PLANT DISEASE RESISTANCE GENES
FILLE REPERENCE: S-70034A
CURRENT APPLICATION NUMBER: US/10/482,526A
CURRENT FILING DATE: 2003-12-18
PRIOR PELICATION NUMBER: US 60/300,112
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 1394
SEQ ID NO 576
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB :
Pred. No. 63;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                              Sequence 576, Application US/10482526A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-10-972-963-70
Sequence 70, Application US/10972963
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVLTRAEGLK 61
                                      432 TRLRRSRG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-482-526A-576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
PCT-US04-35137-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 TRTPRSRGL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRSRGL 9
1 TRLTRSRG 8
                                                                                                                            US-10-482-526A-576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US04-35137-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 70
LENGTH: 388
TYPE: PRT
  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

ò g

```
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Elitra Pharmaceuticals Inc.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034VPC

CURRENT FILING DATE: 2002-03-12

PRIOR PPLICATION NUMBER: PCT/US02/09107B

CURRENT FILING DATE: 2001-03-21

PRIOR PPLICATION NUMBER: 09/948,993

PRIOR PPLICATION NUMBER: 60/342,923

PRIOR PPLICATION NUMBER: 60/342,923

PRIOR PLING DATE: 2001-10-25

PRIOR PLLING DATE: 2001-10-26

PRIOR PLLING DATE: 2002-09

PRIOR PLLING DATE: 2002-09-06

PRIOR PLLING DATE: 2002-03-06

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO S2732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 74744, Application PC/TUS0209107B

GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals Inc.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA,034VPC
CURRENT APPLICATION NUMBER: PCT/US02/09107B
CURRENT PILING DATE: 2001-03-21
CURRENT PILING DATE: 2001-03-21
FRIOR PRICATION NUMBER: 09/948,993
FRIOR FILING DATE: 2001-03-06
FRIOR APPLICATION NUMBER: 00/342,923
FRIOR PILING DATE: 2001-03-06
FRIOR PILING DATE: 2001-03-06
FRIOR FILING DATE: 2001-03-06
FRIOR FILING DATE: 2002-03-06
FRIOR FILING DATE: 2002-03-06
FRIOR FILING DATE: 2002-03-06
FRIOR FILING DATE: 2002-03-06
FRIOR APPLICATION NUMBER: 10/072,851
FRIOR FILING DATE: 2002-03-06
FRIOR APPLICATION NUMBER: 00/362,699
FRIOR APPLICATION NUMBER: 00/362,699
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER: 00/306
FRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                   Score 31; DB 1; Length 522;
Pred. No. 1.4e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31; DB 1; I Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Clostridium botulinum
PCT-US02-09107B-52732
                                          ; ORGANISM: Pseudomonas syringae
PCT-US02-09107B-69335
                                                                                                                                                                                              Query Match 64.6%;
Best Local Similarity 60.0%;
Matches 6; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 TRLORTEGLR 461
                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || ::||||
27 RLLKNRGLK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US02-09107B-52732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
PCT-US02-09107B-74744
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A CURRENT: Elitera Pharmaceuticals Inc.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034VPC
FILE REFERENCE: ELITRA.034VPC
CURRENT APPLICATION NUMBER: PCT/US02/09107B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR PRILING DATE: 2001-02-20
PRIOR PRILING DATE: 2001-02-26
PRIOR PRILING DATE: 2001-02-68
PRIOR APPLICATION NUMBER: 60/342,923
PRIOR APPLICATION NUMBER: 00/362,699
PRIOR APPLICATION NUMBER: 60/362,699
PRIOR APPLICATION NUMBER: 2002-03-06
NUMBER: OSCIOLO3-06-03-06
NUMBER: OSCIOLO3-03-06
NUMBER: OSCIOLO3-03-06
NUMBER: OSCIOLO3-03-06
NUMBER: OSCIOLO3-03-06
NUMBER: OSCIOLO3-06
NUMBER: OSCIOLO3-03-06
NUMBER: OSCIOLO3-06-03-06
NUMBER: OSCIOLO3-03-06
NUMBER: OSCIOLO3-03-06
NUMBER: OSCIOLO3-06-03-06
NUMBER: OSCIOLO3-06-03-06
NUMBER: OSCIOLO3-06-03-06
NUMBER: OSCIOLO3-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-06-03-0
                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                          Score 32; DB 6; Length 441;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.6%; Score 31; DB 6; Length 474; 70.0%; Pred. No. 1.2e+02; Live 1; Mismatches 2; Indels
                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: University of North Carolina-Chapel Hill APPLICANT: Ting, Jenny APPLICANT: Linhoff, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Inhoff, Michael
APPLICANT: Inhoff, Michael
APPLICANT: Hinhoff, Michael
APPLICANT: Hinhoff, Michael
APPLICANT: Hilliams, Kristi
APPLICANT: Lich, John
APPLICANT: Lich, John
APPLICANT: Davis, Beckley
APPLICANT: Davis, Beckley
APPLICANT: Brian
APPLICANT: Shang, Jinghua
APPLICANT: Shang, Jinghua
APPLICANT: Zhang, Jinghua
APPLICANT: Zhang, Jinghua
APPLICANT: Zhang, Jinghua
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Lang, Lickey, W. Jane
APPLICANT: Shang, Jinghua
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Linghua
APPLICANT: Conti, Brian
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICANT: Linghua
APPLICA
                                                                                                                              1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69335, Application PC/TUS0209107B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 167, Application US/10511989 GENERAL INFORMATION:
                     66.7%;
70.0%;
     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 70.0
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                  105 rvirkaEGLK 114
                                                                                                                                                                                                                   1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 TRLTTSKRLK 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-989-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US02-09107B-69335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-511-989-167
```

ð g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
PCT-US02-09107B-51874

j Sequence 51874, Application PC/TUS0209107B

j GENERAL INFORMATION:
    TITLE OF INFORMATION:
    TITLE OF INFORMATION: Identification of Essential Genes in Microorganisms
    PLE REPERENCE: ELITRA. 034VPC

CURRENT APPLICATION NUMBER: PCT/US02/09107B

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 09/948,993

PRIOR PILING DATE: 2001-03-21

PRIOR PLING DATE: 2001-03-66

PRIOR PLING DATE: 2001-02-56

PRIOR PLING DATE: 2001-10-25

PRIOR PLING DATE: 2002-03-06

PRIOR PLING DATE: 2002-03-06

PRIOR PLING DATE: 2003-03-06

NUMBER: 0/362,699

PRIOR PLING DATE: 2002-03-06

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699

NUMBER: 0/362,699
                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                           Query Match 64.6%; Score 31; DB 1; Length 534; Best Local Similarity 66.7%; Pred. No. 1.4e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.6%; Score 31; DB 1; Length 535; Best Local Similarity 66.7%; Pred. No. 1.48+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: December 29, 2004, 13:18:14 Job time : 9.97727 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
PCT-US02-09107B-51874
; ORGANISM: Streptococcus pyogenes PCT-US02-09107B-74744
                                                                                                                                                                                                                          2 RLTRSRGLK 10
                                                                                                                                                                                                                                                                      || ::||||
26 RLLKNRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || ::||||
27 RLLKNRGLK 35
                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
```

THE PARTY OF THE P

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec

US-09-823-418-5 48 1 TRLTRSRGLK 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\* Database

1: pirl: \* 2: pir2: \* 3: pir3: \* 4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	apolipoprotein B -	apolipoprotein B-1			apolipoprotein B-1	conserved hypothet	traX protein - Str	hypothetical 34.6	hypothetical prote		acetyltransferase,	apolipoprotein B-1	ferrous iron trans	apolipoprotein B-1	hypothetical prote	probable phosphopr	starch synthase (E	pathogenicity fact	hypothetical prote	phosphoadenylyl-su	probable threonin	threonine dehydrat	pyruvate dehydroge	hypothetical prote	hypothetical prote	싆	DNA ligase (ATP) (	DNA ligase (ATP) (	cobyric acid synth
SUMMARIES	ID	832802	LPHUB	C60950	JH0102	E60950	AH0906	S39854	E65112	E85985	B91140	G87383	A60950	S75294	JH0101	E72691	S48288	S40051	T18448	E72514	828609	A98146	AC3142	DEHUPT	E83061	B72386	T40901	LQBP34	S06464	AD3338
	DB	7	Н	7	~	ď	0	~	Н	~	~	~	N	Н	N	~	N	~	~	N	-	~	~	-	~	~	~	Н	N	7
	f Query Match Length	596	4563	269	779	275	309	290	309	309	309	173	274	614	784	101	393	484	1838	208	232	304	336	388	412	420	486	487	487	206
•	Query Match	91.7	91.7	83.3	83.3	79.2	77.1	72.9	72.9	72.9	72.9	70.8	70.8	70.8	70.8	68.8	68.8	68.8	68.8	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
	Score	44	44	40	40	38	37	32	32	35	35	34	34	34							32									
	Result No.	-	7	٣	4	2	9	7	80	6	10	11	12	13	14	15	16	17			20									29

hypothetical prote	hypothetical prote	myc-like regulator	UL56 protein - hum	hypothetical prote	hypothetical prote	leucine rich repea	pyruvate formate-1	probable DnaJ prot	CTP synthase (impo	CTP synthetase [im	CTP synthase (UTP-	CTP synthase (EC 6	3',5'-cyclic-nucle	hypothetical prote	hypothetical prote
AB1875	S76027	T14681	C48560	E83363	E84797	T17033	F69534	D96795	C95057	C86686	G97255	F97926	S71626	T05448	S67595
~	N	~	٦	~	0	0	-	7	N	N	~	N	~	N	7
680	1036	146	233	272	290	329	330	398	535	535	535	535	712	732	788
.7	۲.	٠.	œ.	9.	φ.	œ.	9.	9	9.	9.	9.	ų.	9.	9.	٠.
66.7	99	64	64	64.6	64	64	64	64	64	64	64	64	64	64	64
32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31
_	_	~	<u>«</u>	₩.	'n		_	_	_	_		٠.	_	_	

#### ALIGNMENTS

```
apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 332802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchir Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: 532802; MUID:92075708; PMID:1742325
A;Accession: 532802
A;Accession: S32802
A;Accession: Ballinary
A;Residues: 1-596 < PAP>
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301-C;Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 2;
Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0
Matches 9; Conservative
```

# 226 TRLTRKRGLK 235 1 TRLTRSRGLK 10

셤 ઠે

N.Contrains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C; Species: Homo sapiens (man)
C; Species: Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C; Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A26452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R; Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scion 6, 363-372, 1987 apolipoprotein B-100 precursor - human

A,Title: DNA sequence of the human apolipoprotein B gene.
A,Reference number: A27850; MUID:88003974; PMID:3652907
A,Rocession: A27850
A,Rocession: A27850
A,Rocession: A27850
A,Rocession: A27850
A,Rocession: A27850
A,Residues: 1-617, A,' 619-1929, F', 1931-3318,'D', 3320-3426,'T', 3428-3431,'O', 3433-3731, A,Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMNO; UNI-R;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A,Title: The complete sequence and structural analysis of human apolipoprotein B-100: r. A,Recession: A28679

A; Modecule type: mRNA A; Residues: 1-11,15-2539,'8',2541-3823,'R',3825-4563 <CLA> A; Note: 1109-Asp was also found A; Note: 1109-Asp was also found R; Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

```
Contents: disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A28002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A29659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A35783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Molecule type: mRNA
A; Residues: 1-29; ARNA
A; Cross-references: Gs: Motulsky, A.G.; Albers, J.J.
B; Debb, S.S.; Motulsky, A.G.; Albers, J.J.
B; Debb, S.S.; Motulsky, A.G.; Albers, J.J.
B; Debb, S.S.; Motulsky, A.G.; Albers, J.J.
B; Debb, S.S.; Motulsky, A.G.; Albers, J.J.
B; Debb, S.S.; Motulsky, A.G.; Albers, J.J.
B; Dece. Meal. Accession: As2774
A; Reference number: A25774
A; Residues: 709-791, SSSWKAASHGCPHSAGD, BID: 906 <DES
A; Residues: 709-791, SSSWKAASHGCPHSAGD, BID: AAAA1759.1; PID: G178822
A; Residues: 709-791, SSSWKAASHGCPHSAGD, BID: AAAA1759.1; PID: G178822
B; Carlsson, P.; Darnfors, C.; Oldsson, S.O.; Bjursell, G.
A; Title: Analysis of the human apolipoprotein B gene; complete structure of the B-74 reg
A; Residues: 1282-2721, 2742-3290, L', 3292-3336, N', 3338-3948, F', 3950-3963, Y', 3965-4180,
A; Residues: 1282-2721, 2742-3290, L', 3292-3336, N', 3338-3948, F', 3950-3963, Y', 3965-4180,
A; Residues: 1282-2721, 2743-3290, L', 3292-3336, N', 3338-3948, F', 3950-3963, Y', 3965-4180,
A; Residues: 1282-2721, 2743-3290, L', 3292-3336, N', 3338-3948, F', 3950-3963, Y', 3965-4180,
A; Residues: 1282-2721, 2743-3290, L', 3292-3336, M', 3840, N', 3840,
                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Realdues: 1-272, N', 274-617, A', 619-1217, E', 1219-2091, V', 2093-2364, T', 2366-2679, 'Q'
A; Cross-references: GB: XV4506; NID: G34330; PIDN: CAA28191.1; PID: G34331
R; Law, S.W.; Grant, S.M.; H; H; Houchi, K.; Hoppattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID: 87041416; PMID: 3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Molecule type: mRNA

A.Residues: 1-97, 17, 99-328, 7V, 330-644, 17, 646-918, P, 920-3318, D, 3320-3426, T, 3428-94132, 'G', 4134-4180, 'E', 4182-4563 - CHE>

A.Cross-references: GB.J02610, NID:g178803, PIDN:AAA35549.1, PID:g178804

A.Cross-references: GB.J02610, NID:g178803, PIDN:AAA35549.1, PID:g178804

B.Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides R.Protter, A.A., Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; Proc. Natl. Acad. Sci. U.S.A. 33, 5678-5682, 1986

A.Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein A.Reference number: A24320, MUID:86287319; PMID:3461454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 485-617, 'A', 619-1044 <LA2>
A; Residues: 485-617, 'A', 619-1044 <LA2>
A; Residues: 485-617, 'A', 619-1044 <LA2>
A; Ross-references: GB:M12480; NID:g178791; PIDN:AAA51751.1; PID:g178792
B; Protter: A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr A; Reference number: A94088; MUID:86149325; PMID:3513177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Molecule type: mRNA

A.Residues: 1-617, 'A', 619-703,'P', 705-792,'R', 794-1270,'S',1272-1866,'G',1868-2036,'N', 2

A.Residues: 1-617, 'A', 619-703,'P', 705-792,'R', 794-1270,'S',1272-1866,'G',1868-2036,'N', 2

A.Mote: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and

A.Mote: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and

A.F. Chen, S.H., Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M.

J. Biol. Chem. 261, 12918-12921, 1986

A.Title: The complete cDNA and anamo acid sequence of human apolipoprotein B-100.

A.Reference number: A92556; MUID:87008488; PMID:3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-97, 'I', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138, 'PTGRLPNCFSNGLICYSLWIHSFQE
A; Residues: 1-97, 'I', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138, 'PTGRLPNCFSNGLICYSLWIHSFQE
A; Crose-references: Gam4081; NTD:918795; PIDN:AAA51752.1; PID:9553189
B; Crose-references: Gam4081; NTD:940814, 'NTD:958000; J.M.; Sakaguchi, A.Y.; Naylor, Proc. Natl. Acad. Sci. U.S. A. 82, 8340-8344, 1985
A; Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A; Reference number: A24684; MUID:86094221; PMID:3001697
                                                                        human apolipoprotein B-100.
ritie: Complete cDNA and derived protein sequence of PReference number: A93639; MUID:87016385; PMID:3763409 Accession: A25263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: A24684
```

```
Rishoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E., Atherosclerosis 58, 277-289, 1985
Aritie: Molecular cloning of human LDL apolipoprotein B CDNA. Evidence for more than on A; Reference number: A90084; MUID:86130855; PMID:3841481
A; Rolecule type: MRNA
A; Molecule type: MRNA
A; Residues: 3846-4298 <SHO>
B; Pfizzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A; Reference number: A25572; MUID:87076044; PMID:3024665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A25572
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: A339-4563 <PFI>
A;Cross-references: GB:M36676
R;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
A;Reference number: A24738; MUID:86042646; PMID:2932736
A;Accession: A24738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Roceule type: mRNA
A;Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39]
A;Roceule type: mRNA
A;Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39]
A;Crose-references: GB:M12413; NID:9178735; PIDN:AAA51742.1; PID:9178736
B;Chenc. 238, 363-366, 1987
A;Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in A;Reference number: A40133; MUID:88018019; PMID:3659919
A;Recession: B40133
A;Molecule type: mRNA
A;Residues: 2165-2179 cCH1>
A;Residues: 2165-2179 cCH1>
A;Residues: 2165-2179 cCH1>
A;Residues: 515-5179 cCH1>
A;Residues: 51-75;101-10;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55;
A;Molecule type: protein
A;Residues: 51-75;101-10;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55;
A;Note: these fragments were derived from apo48
A;Note: these fragments were derived from apo48
B;Ochem: Biophys: Res: Commun. 149, 121-1219, 13987
A;Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism F
A;Reference number: A28002; MUID:88106542; PMID:3426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     υH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mean and a; Molecule type: molecule the sequence shown represents the carboxyl end of apolipoprotein B-48 A; Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest chencodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA, Ryang, C.; Kim, T.W.; Wengy, S.; Lee, B.; Yang, M.; Gotto Jr., A.M. Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990 A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A; Reference number: A35783; MUID:90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Wolecule type: protein
A;Reaidues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stop codon in human intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 2129-2179, 2181-2235 <HA2>
A; Residues: 2129-2179, 2181-2235 <HA2>
A; Cross references: GB.M18471
A; Experimental source: intestine
A; Note: this mRNA from intestine includes a stop codon created by RNA editing in place
A; Mote: Acids Res. 13, 6937-6953, 1986
Nucleic Acids Res. 13, 6937-6953, 1986
A; Title: Human apolipoprotein B: identification of cDNA clones and characterization of
A; Reference number: A24269; MUID:86041888; PMID:3903660
```

```
Rismith, T.J.

Bubmitted to GenBank, June 1990

A;Reference number: A38864

A;Accession: JH0102

A;Accession: JH0102

A;Accession: JH0102

A;Accession: JH0102

A;Accession: JH0102

A;Cross-references: UNIPROT:Q60536; GB:M35187

A;Cross-references: UNIPROT:Q60536; GB:M35187

A;Cross-references: UNIPROT:Q60536; GB:M35187

A;Cross-references: UNIPROT:Q60536; GB:M35187

A;Title: A;Autamaa, D.; Maeda, N.

Gene 87, 309-310, 1990

A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of an A;Reference number: JH0101; MUID:90236327; PMID:2332175

A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Reywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein P;435-445/Region: receptor binding P;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apolipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B60950
R;Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD: A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: E60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-275 < LAW>
A;Residues: 1-275 < LAW>
C;Coss-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0906
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica
       apolipoprotein B - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0102
R;Smith, T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2
Pred. No. 4.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB;
Pred. No. 3.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Genetics:
A,Gene: apoB
C,Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||| ||||
642 SRLTRKRGLK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 TSĽTRKRĠĽK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                        A.Reference number: A22006, MUID:84208786; PMID:6373369
A.Recession. A22006
A.Roccession. A22006
A.Roccession. A22006
A.Roccession. B22006
A.Roccession. B2006
A.Roccession. B2006
A.Riblackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.; R.Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.; A.Title. Structure of the human apolipoprotein B gene.
A.Reference number: A92564; MIID:87057153; PMID:2946672
A.Contents: annotation; gene structure
R.Ragener, R.; Pfitzner, R.; Stoffel, W.
B.G. Chem. Hoppe-Seyler 386, 419-425, 1987
A.Title: Studies on the organization of the human apolipoprotein B 100 gene.
A.Reference number: A90715; MUID:87271140; PMID:2886136
A.Contente: annotation; gene structure
R.Reigazber, K.H.; Rall Jr., S.C.
J. Bloi. Chem. 262, 11097-11103, 1987
A.Title: Human apolipoprotein B-100 heparin-binding sites.
A.Reference number: A92605; MUID:87280197; PMID:3301850
A.Contente: annotation; heparin binding protein.
A.Reference number: A90125; MUID:66242424; PMID:3087360
A.Contente: annotation; claim binding protein.
A.Reference number: A90125; MUID:66242424; PMID:3087360
A.Contente: annotation; Calium binding protein.
A.Reference number: A90125; MUID:86242424; PMID:3087360
A.Contente: annotation; Calium binding protein.
A.Reference number: A90189
A.Title: And A.Reference number: A90189
A.Title: And A.Reference number: A90189
A.Title: And A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
A.Reference number: A90189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   profise Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C60998
A;Itle: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Accession: C60950
A;Molecule type: DNA
A;Mesidues: 1-269 cLAM>
A;Mesidues: 1-269 cLAM>
A;Residues: 1-269 cLAM>
A;Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.7%; Score 44; DB 1; Length 4563; 90.0%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                       A;Title: Human apolipoprotein B: partial amino acid sequence A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 40; DB 2
80.0%; Pred. No. 1.5;
cive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|||| ||||
216 SRLTRKRGLK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

g

ઠે

ö

Gaps

ö

ö

Gaps

ö

RESULT 4

셤 ઠે

```
|:| | ||||
170 TQLARQRGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetica:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
G87383
                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical 34.6 kD protein in arcB-gltB intergenic region - Bscherichia coli (strain K C;Species: Bscherichia coli C;Species: Bscherichia coli C;Species: Bscherichia coli C;Species: Dependence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: E65112 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc Science 277, 1453-1462, 1997 A;File: The complete genome sequence of Escherichia coli K-12. A;Recession: E65112 A;Recession: E65112 A;Retus: preliminary; nucleic acid sequence not shown; translation not shown A;Recession: E65112 A;Retus: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-309 *ABLAT> A;Cross-references: UNIPROT:P45476; GB;AE000400; GB:U00096; NID:g2367203; PIDN:AAC76243. A;Experimental source: strain K-12; substrain M01655 C;Genetics: A;Gene: yhoc C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
          'Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
'Reference number: AB0502; MUID:21534947; PMID:11677608
'Accession: AH0906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Status: preliminary
A/Molecule type: DNA
A/Rosafdues: 1-290 <BRO>
A/Cross-references: UNIPROT:Q06258; EMBL:X72857; NID:g288432; PIDN:CAA51379.1; PID:g5816
C/Genetics:
A/Start codon: GTG
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enter A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Recession: AH0906
A;Retaus: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <PAR>
A;Residues: 1-309 <PAR>
A;Crose-references: GB:AL513382; PIDN:CAD07846.1; PID:g16504394; GSPDB:GN00176
C;Genetics:
A;Gene: STY3508
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: yhcC
Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trax protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accession: S39654; S32232
R;Brolle, D.F.; Pape, H.; Hopwood, D.A.; Kieser, T.
Mol. Microbiol. 10, 157-170, 1993
A;Title: Analysis of the transfer region of the Streptomyces plasmid SCP2*.
A;Reference number: S39853; MUID:95058174; PMID:7968512
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2; Length 290;
Pred. No. 17;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               Length 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.9%; Score 35; DB 1; Length 309; llarity 70.0%; Pred. No. 18; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                          Score 37; DB 2;
Pred. No. 7;
1; Mismatches 2
                                                                                                                                                                                                                                                                                       77.18;
70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.9%;
87.5%;
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 72.9
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         ||: | ||||
170 TRIARERGLK 179
                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTRSRGLR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
hypothetical protein yhoc [imported] - Escherichia coli (strain O157:H7, substrain EDL93. C.Species: Escherichia coli (C.Species: Escherichia coli (C.S.) (C.Species: Escherichia coli (C.S.) (C.Species: Escherichia coli (C.S.) (C.Species: Escherichia coli (C.S.) (C.Species: Escherichia coli (C.S.) (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Escherichia coli (C.Speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cispecies: Escherichia coli
Cispecies: Escherichia coli
Cibate: 18-Vul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
CiAccession: B91140
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Byasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein BC84090 [imported] - Escherichia coli (strain 0157:H7, substrain RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-309 <HAY>
A,Cross-references: UNIPROT:P45476; GB:BA000007; PIDN:BAB37513.1; PID:g13363563; GSPDB:C
A,Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acetyltransferase, GNAT family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: 687383
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: yhcC
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: EC94090
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.9%; Score 35; DB 2; Length 309; Best Local Similarity 70.0%; Pred. No. 18; Matches 7; Conservative 1; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.9%; Score 35; DB 2; llarity 70.0%; Pred. No. 18; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 TOLARORGIK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 rolakokcik 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserv?
```

```
C'Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C'Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C'Accession: JH0101, 833128; D60950
R'Smith, T.J.; Hautamaa, D.; Maeda, N.
R'Smith, T.J.; Hautamaa, D.; Maeda, N.
A'Smith, T.J.; Houtamaa, D.; Maeda, N.
A'Title: Sequence of the putative low-density lipoprotein receptor-binding regions of as A'Reference number: JH0101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A,Reference number: A60950; MUID:90324804; PMID:2373361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AjGene: MGI:Apob
AjCross-references: MGI:88052
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,
F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; i. 180A Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy. A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA*
A,Rosaidues: 1-101 AKAN-
A;Cross-references: UNIPROT:Q9YDG4; DDBJ:AP000060; NID:g5104188; PIDN:BAA79933.1; PID:g
A;Experimental source: strain K1
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein APE0949 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                      Gaps
                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                   Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                      DB 1;
56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2;
Pred. No. 71;
1; Mismatches
                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GB:M35186
                                      Score 34;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Accession: JH0101
A.Molecule type: DNA
A.Residues: 1-784 <SMI>
Cross-references: UNINOT:Q61314; GB:M35186
R.Smith, T.; Hautamaa, D.; Maeda, N.
submitted to the EMBL Data Library, May 1989
                                                                                                                                                                                                                                                                                                                                                                                 apolipoprotein B-100 - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 427-531,'S',533-700 <LAW>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Reference number: 833128
A, Accession: 833128
A, Accession: 833128
A, Molecule type: DNA
A, Residues: 1-531,'S', 533-784 <SM2>
A, Cross-references: EMBL:X15191
R, Law, A, Scott, J.
J, Lipid Res. 31, 1109-1120, 1990
                                      70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.v.
                                                                                                   6; Conservative
                                                                                                                                                                                                    361 TRVMRSRGMR 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 SRLMRKRGLK 656
                                                                                                                                                             1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRSRGLK 10
                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: E72691
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: D60950
                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
E72691
                                                                                                                                                                                                                    원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein B-100 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 0ryctolagus cuniculus (domestic rabbit)
C;Species: 0ryctolagus cuniculus
C;Species: 0ryctolagus cuniculus
C;Species: 0ryctolagus cuniculus
C;Species: 0.0000
R;Law, A.; Scott, J.
L; 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Reference number: A60950; MUD:90324804; PMID:2373961
A;Reference number: A60950
A;Residues: 1-274 < LAW>
A;Residues: 1-274 < LAW>
A;Cross-references: UMIPROT:O/M2U9
A;Cross-references: UMIPROT:O/M2U9
A;Cross-references: UMIPROT:O/M2U9
A;Cross-references: UMIPROT:O/M2U9
A;Cross-references: UMIPROT:O/M2U9
A;Cross-references: UMIPROT:O/M2U9
C;Superfamily: apolipoprotein B
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S75294
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: 874322; MUID:97061201; PMID:8905231
A,Accession: 875294
A;Accession: 875294
A;Accession: 875294
A;Accession: S75294
A;Accession: S75294
A;Accession: S75294
A;Accession: Number and a sequence not shown; translation not shown
A;Accession: 1-614 cKAN>
A;Accessive type: DNA
A;Accessive type: DNA
A;Accessive the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Accessive feob
A;Gene: feob
C;Superfamily: ferrous iron transport protein B; translation elongation factor Tu homolo
C;Superfamily: ferrous iron transport protein B; translation elongation factor Tu homolo
C;Keywords: GTP binding; nucleotide binding; P-loop
F;19-134/Domain: translation elongation factor Tu homology cETU>
F;25-32/Region: nucleotide-binding motif A (P-loop)
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87383
A;Status: preliminary
A;Molocule type: DNA
A;Residues: 1-173 <STO>
A;Cross-references: UNIPROT:Q9A9B1; GB:AE005673; NID:g13422385; PIDN:AAK23067.1; GSPDB:CGGenetics:
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ferrous iron transport protein B - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein s1r1392
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S75294
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.8%; Score 34; DB 2; Length 274; 87.5%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 173;
Pred. No. 17;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                           70.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                              Query Match 70.8
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 TRLMRARGL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 LTRKRGLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRSRGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

C;Genetics: A;Gene: APE0949 C;Superfamily: Aeropyrum pernix hypothetical protein APE0949

0; Gaps Query Match 68.8%; Score 33; DB 2; Length 101; Best Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels

0,

3 LTRSRGL 9 ||||||| 74 LTRSRGL 80

ð a

Search completed: December 29, 2004, 12:39:03 Job time : 10.6591 secs

Q8fd65 escherichia Q8fd65 streptomyce Q8vwd2 streptomyce Q8vwd2 streptomyce Q8vd3 streptomyce Q3bjfc shigella f1 Q83jfc shigella f1 Q88c72 pseudomonas Q98kj7 pseudomonas Q98kj7 pseudomonas Q98kj7 pseudomonas C938k candida boi G6nac6 rhodopseudo Cae26702 rhodopseu

O52565 amycolatops Q8fd65 escherichia

Aas07756 amycolato Q7bud9 amycolatops

OM protein

ö

Run

Sequence:

Searched:

Database

Result Š. 

```
Actus vociferans (Spix's owl monkey).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.,

"A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.",

Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apolipoprotein B (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Liver;
WREDLINE-29075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45955 MW; EEFA8492157E1BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2
Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                            414 AA
                                                                                                                                                                                                                                     ALIGNMENTS
                          052565
08FD65
006258
08VWD2
YHCC_ECOLI
08UBF4
083JF2
088C72
                                                                                                                                                            DAS CANBO
QENACE
             AAS07756
                                                                                                                                                                                         CAE26702
                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                            PRT;
Q7BUD9
                                                                                                                                                                                                                                                                                                                                                                               Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 25, C
(TrEMBLrel. 25, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
90.0%;
                             0000-0000
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
4430
4330
4330
4330
4467
4467
4467
4467
4467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 TŘĹŤŘKŘĠĽK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein.
NON TER
NON TER
SEQUENCE 41
                                                                                                                                                                                                                                                                                                                         Q7YQR5;
01-OCT-2003 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003
 \alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q28473
Q28473;
                                                                                                                                                                                                                                                                                                            Q7YQR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                RESULT 1
 Q7YQR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028473
                                                                                                                                                                                                                                                                                                               SETT WERE REPORTED TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rousettus a
chaetophrac
agouti paca
hydrochoeru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ornithorhyn
tachyglossu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arabidopsis
arabidopsis
arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glaucomys v
diceros bic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           streptococc
phalanger o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nyctimene a
pteropus hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erethizon d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dinomys bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atherurus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macaca fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mesocricetu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mesocricetu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hystrix bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yarrowia li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                December 29, 2004, 12:13:11; Search time 58.4091 Seconds (without alignments) 98.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               072600
074168
077410
077410
077410
077704
077104
071171
060334
060334
060337
060337
060337
071877
080403
077470
077470
077470
077470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6C494
Q9fxm2
Q818t0
Q91va4
Q98e60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7tn65
Q7tn69
                             Compugen Ltd.
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q28473
Q13788
APB_HUMAN
Q72600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07TN68
07YR10
07YQM8
07YQM7
07YR04
07YR08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7TN72
Q60537
Q60537
Q60537
Q7YQM2
Q7YQM9
Q7YW00
Q7TN70
Q7TN65
Q7TN65
Q7TN65
Q6C494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8L8T0
Q9LVA4
Q98E60
                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                          UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                             US-09-823-418-5
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                         1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400
405
445
                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
```

ö

Gaps

P,

```
B-100: relationship between apps-100 and apoB-48 forms.";
EMBO J. 5:3495-3507(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE-87008481, PubMed=3759943;
Chen S.-H., Yang C.-X., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 3109-4563 FROM N.A.
MEDLITE=8500528; PubMed=2994225;
Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
Mahley R.W., Scott J.;
"Human apolipoprotein B. structure of carboxyl-terminal domains, sites
of gene expression, and chromosomal localization.";
[10]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [7]
SEQUENCE OF 3056-3159 FROM N.A.
MEDLINE=86641888; PubMed=3903660;
Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgesener T.G., Lin H.-C., Wang X., Ma Y., Mendlaz B., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNN.";
                                                                                                                        MEDLINE-87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.,
"Complete cDNA and derived protein sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
MEDINTE-86693680; PubMed=3841204;
Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
Bjursell G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.;
"Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
derived amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE-88003974; PubMed=3652907;
Ludwig E.H., Blackhart B.D., Flerotti V.R., Caiati L., Fortier C
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-87161758; PubMed=3030729;
Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
VCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=85270450; PubMed=3860836;
MEDLINE=85270450; PubMed=3860836;
Deeb S.S., Motulsky A.G., Albers J.J.;
"A partial cDNA clone for human apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning of human apolipoprotein B cDNA.";
Nucleic Acids Res. 13:8813-8826(1985).
                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 14:7501-7503 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 261:12918-12921(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 13:6937-6953(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA 6:363-372(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zannis V.
                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APB HUMAN STANDARD; PRT; 4563 AA.
P04114; 000502; Q13787;
01-N0V-1986 (Rel. 03, Created)
01-N0V-1986 (Rel. 03, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-100 precursor (Apolipoprotein B-100 precursor (Apoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-87191999; PubMed=2881086; Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.; "Analysis of the human apolipoprotein B gene; complete structure of Gene 49:29-51(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
   "Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 2; Length 3262;
Pred. No. 15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                               the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56603BC0618DD40D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M15421; AAA51758.1; -.
PIR; A27850; LPHUB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
GO:0006869; P:lipid transport; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2;
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 3262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24, APOB protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.7%;
90.0%;
                                                                                                                                                                                                              Murray R.;
Submitted (FEB-1992) to th
EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2084 İRLİRKRİĞİK 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 TRLTRKRGLK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                            596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3262 AA;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          1
596
                                                                                                                                                                                rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                             Lipoprotein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=APOB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q13788
Q13788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APB_HUMAN
   RTT REPRESENT THE STATE OF STATE STATE OF STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCOCCOS ON THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OS GE DIT ACT
```

```
Q7Z600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               072600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07Z600
 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
          MEDLINE-86149325; PubMed=3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.; "Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100.";
Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 oŧ
                                                                                                                                                                                                                           PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
MEDIATE=88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
Gotto A.M., Dir, Li W.-H., Chan L.;
Apolipoprotein B-48 is the product of a messenger RNA with an organ-
epecific in-frame stop codon.;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
Levy-Wilson B., Scott J.;
"Complete protein sequence and identification of structural domains
human apolipoprotein B.";
                                                                                                          SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE=86287319; PubMed=3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.; "Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene."; Hum. Genet. 86:91-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89098975; PubMed=2563166;
Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20143590; PubMed=10679026; Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.; Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and triglycerides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprochen B is a calcium binding protein.";
Biochem. Biophye. Res. Commun. 137.493-499(1986).
                                                                 apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682 (1986)
[12]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Cell 11:721-734(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91071750; PubMed=1979313;
SEQUENCE OF 1-291 FROM N.A.
                                                                                                                                                                                                                                                                                                                                Science 238:363-366(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALMITOYLATION OF CYS-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 323:734-738(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALCIUM-BINDING DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANT FDB GLN-3527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT SER-4338
                                                                                                                                                                                                                                                                                                                                                              DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAINS,
```

```
MEDLINE-97403938; PubMed-9259199;
Rabes J.P., Varret M., Saint-Jore B., Brlich D., Jondeau G.,
Krempf M., Giraudet P., Junien C., Boileau C.;
Framilial ligand-defective apolipoprotein B-100: simultaneous
detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a French

    Hun. Genet. 102:44-49(1998).
    FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
    SUBCELLULAR LOCATION: Secreted.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                             MEDILINE-55190020; PubMed=7883971; Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.; "Familial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity."; J. Clin. Invest. 95:1225-1234(1995).
                                                                                                                                                                                                                                                                                                                                                                       VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poirier O., Ricard S., Behague I., Souriau C., Evans A.E., Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.; "Detection of new variants in the apolipoprotein B (Apo B) gene by
MEDLINE-91016974; PubMed=2216805; Manang Li.-S., Gavish D., Breslow J.L.; "Radague.-S., Gavish D., Breslow J.L.; "Sequence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDININE-8141125; PubMed=9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
hypocholesterolemia."
Hum. Genet. 102:44-49(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C., Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A., Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
Apolipoprotein B (Including Ag(X) antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS FDB GLN-3527 AND CYS-3558.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97044521; PubMed=8889592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hum. Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.7%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hum. Mutat. 8:282-285(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRSRGLK 10
                                                                                                                                     VARIANT FDB CYS-3558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                        AND THR-4481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND ILE-3921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR-SSCP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

.. 0 4

ö

Gape

ö

ò g

```
SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madean H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeson H., Koepfli K.-P., Wayne R.K., Springer M.S.;
H. new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AFS48435; AAP97391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nyctimene albiventer (Common tube-nosed fruit bat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pteropus hypomelanus (Small flying fox).

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;

Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodiae;

Pteropodiane; Pteropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
MEDLINE=22761261; Noopfil; K.-P., Wayne R.K., Springer M.S.;
Marine-Madsen H., Koepfil; K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.",
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                      Score 40; DB 2; Length 432;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%; Score 40; DB 2; Length 436;
80.0%; Pred. No. 11;
cive 1; Mismatches 1; Indels
                                                                                                                                 432
48171 MW; F27B7AB39604732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 1
436 436
436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AA.
                                                                                                                                                                                                                                                                          1; Mismatches
                    Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AY243375; AAP50763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT:
                                                                                                                                                                                                                83.3%;
                                                                                                                                                                                                                                          Local Similarity 80.0 les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pteropodinae; Nyctimene.
NCBI TaxID=48988;
                                                                                                                                                                                                                                                                                                                                                                              275 SRLTRKRGLK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||| ||||
279 SRLTRKRGLK 288
                                                                                                                                                                                                                                                                                                                               1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRSRGLK 10
                                                                                                                                                           432 AA;
                                                                            Lipoprotein.
NON_TER
NON_TER 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=apoB-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein.
NON TER
NON TER
SEQUENCE 43
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7YQM7
                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7YQM7
                    STIXE
                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCOCCOS OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVICE OF THE SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Glaucomys volans (Fragment)
Glaucomys volans (Southern flying squirrel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22761261; PubMed=12878460; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; "A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
10-0CT-2003 (TrEMBLrel. 25, Last sequence update)
Apolipoprotein B (Fragment).
Diceros bicornis (Black rhinoceros).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.,
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.,
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                         Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 40; DB 2; Length 421;
80.0%; Pred. No. 11;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                         4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
46747 MW; D47B77BD4F864FD1 CRC64;
EMBL, AY324608, AAP72970.1; -. GO, GO:00519; F:11pid transporter activity; IEA. GO; GO:0005819; F:11pid transport; IEA. InterPro; IPR0009454; DUF1081.
InterPro; IPR001747; Lipid_transport_N. Pfem; PF06448; DUF1081.
Pfem; PF06448; DUF1081; 1. Pfem; PF06448; Vitellogenin_N; 1. SMART; SM00638; LPD_N; 1.
                                                                                                                                                                                                                                                                                                                   Score 44; DB 2;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 AA
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                             91.7%;
90.0%;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3385 řŘLTŘKŘGĽK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 SRLTRKRGLK 273
                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=64683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein.
NON TER
NON TER
SEQUENCE 42
                                                                                                                                                                                                                                 Lipoprotein.
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7TN68
Q7TN68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7YR10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07YR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
```

ð

ACCOCCOCC OS REPRESENTATION OF THE PROPERTY OF

ö

ö

Gaps

ö

STTTS

RESULT 10

ઠ 셤

```
SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22761261; PubMed=12878460;
Marine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.",
Mol. Phylogenet. Evol. 28:225-240(2003).
Mal. Phylogenet. Evol. 28:225-240(2003).
InterPro: IPR00871; Beta lactamase A.
PROSITE; PS00146; BETA_LACTAWASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                 Agouti paca (Paca).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Agoutidae, Agouti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein B (Fragment).
Mydrochoevus hydrochaeris (Capybara) (Carpincho).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.3%; Score 40; DB 2; Length 445; 80.0%; Pred. No. 11; 11dels ive 1; Mismatches 1; Indels
                                Length 445;
                                                                     Indels
445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;
                                                                                                                                                                                                                                                           01-00T-2003 (TrEMBLrel. 25, Created)
01-00T-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                Match 83.3%; Score 40; DB 2; Local Similarity 80.0%; Pred. No. 11; es 8; Conservative 1; Mismatches
                                                                                                                                                                                                                              445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 AA
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                Apolipoprotein B 100 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 80.(
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                      288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 SRLTRKRGLK 297
                                                                                                    1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=108852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein.
NON_TER
NON_TER 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein.
NON TER
NON TER 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrochaeris
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7TN71;
                                                                                                                                                                                                                              Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                   Matches
                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                              Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C7TTV
                                                                                                                                        셤
                                                                                                                                                                                                                                g
                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-2761561, bubMed=12878460,

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for euchbraian relationships.";

Mol. Phylogenet. Bvol. 28:225-240(2003).

EMBL, AY243383; AAP50771.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  Rouseftus amplexicaudatus (Common rousette).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;

Pteropodinae; Rousettus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Chaetophractus villosus (South American armadillo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Edentata, Dasypodidae, Chaetophractus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-22761261; PubMed=12878460;
Amrine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AX243378; AAP50766.1; -.
                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                  83.3%; Score 40; DB 2; Length 438;
80.0%; Pred. No. 11;
tive 1; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%; Score 40; DB 2; Length 438; 80.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                              1
438
48734 MW; 2BD85BCBF4E2CC41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48597 MW; 41C890DEAF95C872 CRC64;
                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                                 438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
EMBL; AF548436; AAP97392.1;
                                                                                  Query Match
Best Local Similarity 80...
Best Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
+38 438
438 AA; 48F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                               :|||| ||||
281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|||| ||||
281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1445
                                                                                                                                                                         1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRSRGLK 10
                                1
438 4
438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=29080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein.
NON TER
NON TER 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
                  ipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
NON TER
SEQUENCE
                                                   NON TER
SEQUENCE
                                NON TER
                                                                                                                                                                                                                                                                                                                  Q7YR04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7YR08
                                                                                                                                                                                                                                                                                                Q7YR04
```

RESULT 11 Q7YR08

A PART TERMINATION OF THE PRINCE OF THE PRIN

d

ò

ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=90236327; PubMed=2332175;

MEDLINE=90236327; PubMed=2332175;

MEDLINE=90236327; PubMed=2332175;

Macda N.;

"Sequence of the putative low-density lipoprotein receptor-binding regions of apolipoprotein B in mouse and hamster.";

Gene 87:309-310(1990).

Park; M35187; AAA37059.1; -.

PIR; G60950; G60950.
                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragman annotation update)
Brethizon dorsatum (North American porcupine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Erethizontidae;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AY243368; AAP50756.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q60536;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hamster apolipoprotein (apoB) (Fragment).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
   Score 40; DB 2; Length 445;
Pred. No. 11;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 40; DB 2; Length 445; 80.0%; Pred. No. 11; indels .ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445
49617 MW; 9572FE5F5E7625F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           780
86625 MW; E371D1B2079D8F7E CRC64;
                                                                                                                                                                 445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                 PRT;
   83.3%;
Query Match
Best Local Similarity 80.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                           :|||| ||||
288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||| ||||
288 SRLTRKRGLK 297
                                                           1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRSRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
780 7
780 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 AA;
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=34844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein.
NON TER
NON TER 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                              Q7TN72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  060536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
Q60536
                                                                                                                                  RESULT 14
Q7TN72
                                                                                                                                                               ò
                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            요
```

Search completed: December 29, 2004, 12:37:32 Job time : 59.5202 secs

Apolipopr Apolipopr Human apo Human apo Human apo Human apo

Apo-B100 Apo-B100 Apo-B100 Apo-B100 Apo-B100 Apo-B100 Apo B 100 Analogue

Adf43408 Adh18871 Adh18871 Adh33445 Add33445 Add33184 Ady30682 Ady30684 Ady30689 Ady30699 Ady30699 Ady30699 Adw57206 Adw

Apoprotei Human apo

Aae21732 E Abu07938 A Adf56451 E Aaw41260 A Aaw87717

BSMR effe

١.

```
ADF43408
ADH18871
ADH18871
ADD33445
AD333447
AAX30686
AAX30686
AAX30689
AAX30689
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX30690
AAX
  ABU79140
  9911.8
9911.8
9911.8
9911.8
9911.8
9911.8
9911.6
9911.6
9911.6
    December 29, 2004, 12:10:41; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                         2002273 seqs, 358729299 residues
                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                               US-09-823-418-6
49
                                                                                                                                                                                                                                                                                         1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                        BLOSUM62
```

## ALIGNMENTS

	RESULT	NT 1
	AAY	
	<b>?</b>	AAY30687 BTandard; peptide; lu AA.
	<b>4</b> 2	ABY30687;
	×	
	TO	17-NOV-1999 (first entry)
	Χ¦	
	OS C	Apo-B100 derived peptide showing a proteoglycan receptor mutation
	\$ 3	Dro-B100. proteoglycen recentor mitation. atherogolerogie.
	Z.	The density lipoprotein; proteoglycan; LDL; atherosclerotic lesi
	XX	
	SO	Synthetic.
	SO	Homo sapiens.
	×	
	PN	WO9946598-A1.
	ž	
	PD	16-SEP-1999.
	×	
	PF	05-MAR-1999; 99WO-US004805.
	×	
	PR :	10-MAR-1998; 98US-0077618P.
	X	
	PA	(REGC ) UNIV CALIFORNIA.
	X	
	PI	Innerarity TL, Boren JOS;
	X	
	KO :	WPI; 1999-551509/46.
	×	
	ᅜ	Identifying compounds which affect binding of low density lipopi
	PŢ	with proteoglycan, used for, e.g. obtaining compounds for reduci
	PT	atherosclerosis.
	×	
	PS	Claim 17; Page 57; 70pp; English.
	×	
	ខ្ល	AAY30582-Y30700 represent apo-B100 derived peptides showing prot
	ຍ	receptor mutations. They were created to identify compounds which
	ខ្ល	modulate atherosclerosis. The peptides are derived from amino ac
	ខ	to 3367 of apoB100. The method comprises detecting compounds whi
	ខ	low density lipoprotein (LDL) binding with proteoglycan (PG). The
	႘	can be used for identifying compounds which disrupt LDL-PG bindi
	ပ္ပ	without inhibiting LDL receptor binding. Such compounds can be a
	ပ္ပ	reduce or prevent the formation of atherosclerotic lesions and I
	ខ	atherosclerosis. The transgenic non-human animals and mammals wi
	ပ္ပ	express human apo-B100 can be used as an in vivo model system ic
	႘	study of atherosclerosis, and in vivo assay methods for identify
_	ខ្ល	compounds which modulate atherosclerosis and/or LDL-PG binding.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Maximum Match 100% Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Scoring table:

Searched:

Perfect score:

Run on

Sequence:

A\_Geneseq\_23Sep04:\*

Database

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003bs:\* geneseqp2003bs:\*

SUMMARIES

В

Query Match Length

Score

Result No.

Apo-B100 Apo-B100 Apo B bin Apo B 100

Description

Apolipopr ApoB-100

Human apo Nucleic a Peptide #

Aay30687 Aay30682 Aaw37082 Aaw41261 Aaw41261 Aaw57209 Aae14541 Aaw96876 Aaw96876 Aaw96876 Aaw96876 Aaw96876 Aaw96876 Aaw96876 Aaw96876 Aaw3401 Aay31237

Nucleic a

Human liv Human apo

Sequence

Human apo Human Apo

Human apo Human ali

duman abo Amino aci

Heparin b Apo B 100 Apo B 100 Human apo

ABJ37575 AAW57208 AAW57209 AAE14541

AAW57205 AAW57207 AAW41261

AAW96892

10 110 113 113 125 225 337 314

AAW96876 AAW64587 AAW96845

0000 01000 011000 01100 01100 01100 01100 01100 01100 01100 01100 011000 01100 01100 01100 01100 01100 01100 01100 01100 011000 01100 01100 01100 01100 01100 01100 01100 01100 011000 01100

ABB37687

ABG52504 AAR72704 AAR34031

AAY31237 AAW41262

343 3443 3477 3463 3463 3463 4456 4560 4563 4563

AAW96826

ADD48677 AA015893 ABR40253

ion. ä.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate artheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atheroselerosis, and in vivo sassy methods for identifying compounds which modulate atheroselerosis and/or LDL-PG binding. They can

us-09-823-418-6.rag

Sequence 10 AA;

ö

Gaps

.

```
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                  Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                          Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                      100.0%; Score 49; DB 2; Length 10; larity 100.0%; Pred. No. 0.019; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   AAY30682 standard, peptide, 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0077618P
                                                                                                                                                                                                                                                                                    17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                    1 TRLTRORGLK 10
                                                                                                                                                                            TRLTRORGIK 10
                                                                                           Query Match
Best Local Similarity
10; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis.
                                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                        WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1999.
                                                                                                                                                                                                                                                             AAY30682;
                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                 8888888888
                                                                                                                                                     ò
                                                                                                                                                                           셤
```

```
AAY30582-Y30700 represent apo-Blo0 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which computations. They were created to identify compounds which method computed are derived from amino acids 3388 to 3367 of apobl00. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding with proteoglycan (FG). The method compounds to the transpagnic on-bunan animals and mammals which express human apo-Blo0 can be used to atherosclerosis. The transpagnic non-human animals and mammals which express human apo-Blo0 can be used as an in vivo model system for the express human apo-Blo0 can be used as an in vivo model system for the cutounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in can be used to identify compounds which result in an increase in can also be used to atherosclerosic and to end the assays may be used to determine whether form atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
```

```
The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that Las at least 1 binding site for an apo B protein receptor and at least 1 ilpophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KABYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media sepecially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide binding to apo B protein delivering drugs to cancer cells
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
      Length 10;
                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB 2; Length 11;
Pred. No. 0.12;
1; Mismatches 0; Indels
   Score 46; DB 2;
Pred. No. 0.069;
                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.
                                                                                                                                                                     AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 52; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baillie
93.9%;
                                                                                                                                                                                                                                                              Apo B binding site peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.8%;
90.0%;
                                                                                                                                                                                                                              03-AUG-1998 (first entry)
                               9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                            1 TRLTRORGLK 10
                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
                                                                                ||||||:||||
TRLTRERGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TRLTRKRGLK
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                       WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                    AAW57205;
 Query Match
                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                        RESULT 3
                                                                                                                                                      AAW57205
                                                            ઠ
                                                                                        g
                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

Synthetic.

AAW57207;

AAW57207

```
This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). 21-KAQ-XI-KXAKHRHS-X2-T-22 (I) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (as); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as . Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. thibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits callular differentiation or apoptosis. KRAD-14, which is active of the prothrombinase complex; and prevents activation of the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                          Anti-coagulant, apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14; prothrombinase complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.8%; Score 45; DB 2; 90.0%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW96892 standard; peptide; 15 AA.
                                                                Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                    97WO-GB001255
                                                                                                                                                                                                                                                                                                                                                                                                                                 96GB-00009702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ettelaie C;
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 90.0
hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||:||||
TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
                     19-MAY-1998
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                          WO9743311-A1
                                                                                                                                                                                                                                                                                                                                                                                  09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                       20-NOV-1997.
                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) batticle of the present invention. The LDL particle comprises at least peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least of invention are peptides containing an apo B binding sequence with a least of invention are peptides containing an apo B binding sequence with a least of invention are peptides containing an apo B binding sequence with a least of cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                                          Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                  Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 2;
Pred. No. 0.14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baillie G;
                                                             AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-GB002610,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that express this receptor.
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TRLTRKRGLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1997;
                                                                                                                                                     03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
G
```

Halbert

ö

Gaps

ö

Length 15; 0; Indels Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;

AAW41261;

RESULT 5

g ð

AAW41261

Matches

ApoB-100 nuclear localisation signal sequence, residues 3353-3367.

4

WO9856938-A1 17-DEC-1998

Guevara JG,

us-09-823-418-6.rag

```
The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                               Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDb; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 6;
Pred. No. 0.2;
1; Mismatches (
                                                                                                           Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW57208 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                            Disclosure, Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baillie
                                                                                                         Hubbell JA, Schoenmakers R,
             20-JUL-2001; 2001US-0306726P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
9; Conserv?
                                                                                                                                               WPI; 2003-300420/29.
                                                 (ETHZ-) ETH ZUERICH (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-APR-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.8%; Score 45; DB 2; Length 15; larity 90.0%; Pred. No. 0.15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                  Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                97US-00874807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUL-2002; 2002WO-US023419.
                                                                                                                                                                                                                                                                                                                              Hoogeveen RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003007689-A2
                                                                                                                                                                                                                              13-JUN-1997;
14-MAY-1998;
                                                                               Homo sapiens
                                                                                                                                                                                           10-JUN-1998;
```

Query Match Best Loc Matches

g

à

Unidentified

30-JAN-2003

10-MAY-2003

ö

Gape

ö

ö

Length 20; Indels

```
856666666666655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                     after present Bequence represents a special service and set as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KABYKKNKHRH (1) or TRLTRKRGKK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives occurring, receptor-competent LDL particles are brotein receptor, and (iii) additives occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)
                                                                          present sequence represents a specifically claimed Apo B 100 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide binding to apo B protein
delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.8%; Score 45; DB 2; Length 22; 90.0%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-natural lipid particle comprising
receptor - useful as, e.g. vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                 to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Owens MD, Baillie G;
                     Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57209 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||||||
TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
Les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNIN ( TSYU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAWS7209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW57209
```

셤

ઠે

```
ö
particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KADYKKWRHRH (1) or TTRLTRKRGLK (2), or their useful as: (i) drug-targeting veceptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDE), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDE. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDE, in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                2; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                            Score 45; DB 2;
Pred. No. 0.22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE14541 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                            91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yla-Herttuala S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ARKT-) ARK THERAPEUTICS LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-179777/23.
                                                                                                                                                                                                                                                                                                    Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200206314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Narvanen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide p62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE14541;
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE14541
```

Θ

TRLTRKRGLK 20

11

硆

ö

```
Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein sequence can be used in the composition of the invention. The present specification describes a composition of the invention. The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in viro, for expressing a therapeutic polypeptide or antisense cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                              Gaps
                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                     Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                Length 34;
                                                                                                           0; Indels
                                                                            DB 5;
                                                                                          0.33;
                                                                           Score 45; DB Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore JP;
                                                                                                                                                                                                                                  AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Fig 12C; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                     Query Match

Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00874807.
98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guevara JG, Hoogeveen RC,
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.07
                                                                                                                                 1 TRLTRORGLK 10
                                                                                                                                                   25 TRLTRKRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-070331/06.
                                              Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 AA;
                                                                                                                                                                                                                                                                                           22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998
                                                                                                                                                                                                                                                             AAW96876;
                                                                                                                                                                                                      RESULT 11
AAW96876
 8223
                                                                                                                                                                                                                                              ò
                                                                                                                                                           셤
```

```
CC used with Factor V protein fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are vein thrombosis), mutations in apolipoprotein (apo) genes (certain allels of apos indicates increased risk of developing Alzhaner's allels of apos indicates increased risk of developing Alzhaner's allels of abosisted with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method does not require complex apparatus for polymerase chain reactions, it is simple, standardisable and reliable and is particularly suited to routine screening. It also allows mutant protein a sample to be quantified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.
                                                                                                                                Factor V, human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 2; Length 37;
Pred. No. 0.35;
1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                  Human apolipoprotein peptide fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Schenk V;
AAW64587 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                              Lang H,
                                                                                                                                                                                                                                                                                                                          98EP-00890007.
                                                                                                                                                                                                                                                                                                                                                          97AT-00000044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.8%;
90.0%;
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.00,
                                                                                                                                                                                                                                                                                                                                                                                                                        Moritz B, Kiessig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rkirkkicik 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-416142/36.
                                                                                                                                                                                                                                                                                                                                                                                        (IMMO) IMMUNO AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37 AA;
                                                                   23-OCT-1998
                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                      12-JAN-1998;
                                                                                                                                                                                                                                                      BP857973-A2.
                                                                                                                                                                                                                                                                                        12-AUG-1998.
                                   AAW64587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        디
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
```

ö

Gaps

; 0

DB 2; Length 36; 0; Indels

Score 45; DB 2; Pred. No. 0.35; 1; Mismatches

91.8%;

ï

ô

AAW96845 standard; peptide; 51 AA. AAW96845 ID AAWS

TRLTRORGLK 10

ò

```
WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                             26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG52504;
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                      AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apob-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein (VLDL), intermediate density lipoprotein sequence can be used in the composition of the invention. The sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                         Human apolipoprotein B-100, apoB-100; very-low density lipoprotein; VLDL, apollopprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinom; diabetes; arteriosclexosis.
                                                                                                                                                                                                                                                                                                                       Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #5193 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.8%; Score 45; DB 2; Length 51; 90.0%; Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.48
1; Mismatches
                                                   Nucleic acid binding domain from apoB-100
                                                                                                                                                                                                                                                                              Moore JP;
                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 151; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB37687 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                      97US-00874807.
                                                                                                                                                                                                98WO-US011927.
                                                                                                                                                                                                                                                                              Hoogeveen RC,
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [||||:||||
TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                   WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 51 AA;
                                                                                                                                                    WO9856938-A1
                                                                                                                                                                                                  10-JUN-1998;
                                                                                                                                Homo sapiens
                                                                                                                                                                                                                      13-JUN-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                22-APR-1999
                                                                                                                                                                            17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2002
                                                                                                                                                                                                                                                                              Guevara JG,
                                                                                                                                                                                                                                                                                                                                              treatment.
           AAW96845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB37687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
ABB37687
ઠ
```

```
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.8%; Score 45; DB 4; Length 343; 90.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 31152.
                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG52504 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                   ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312P.
2000US-0207456P.
2000US-00632346.
2000US-0234687P.
2000US-0234687P.
2000US-023458P.
                                                                                                         30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0053236c.
21-SEP-2000; 2000US-023687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 90.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 TRLTRKRGLK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                               Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 343 AA;
```

(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2001-488898/53

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

Claim 27; SEQ ID NO 31152; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult 12. Inver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. CC (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlippidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59330 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published\_pot\_sequences 

Gapa ö Match 191.8%; Score 45; DB 4; Length 343; Local Similarity 90.0%; Pred. No. 2.7; es 9; Conservative 1; Mismatches 0; Indels Query Match

ö

1 TRLTRORGLK 10 ò 셤

169 TRLTRKRGLK 178

Search completed: December 29, 2004, 12:28:49 Job time : 62.0227 secs

Sequence 343 AA;

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-6 49

1 TRLTRORGLK 10 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	apolipoprotein B -		apolipoprotein B-1		hypothetical 34.6	hypothetical prote		-H	conserved hypothet	starch synthase (E	hypothetical prote	apolipoprotein B-1	probable phosphopr	apolipoprotein B-1		dihydroorotase (dh	cobyric acid synth	hypothetical prote	soluble starch syn	starch synthase DU	pyruvate formate-1	hypothetical prote	adenylate transloc	starch synthase (E	glycogen synthase	starch synthase (E		DNA	replicative DNA he
	ព	S32802	LPHUB	C60950	JH0102	E65112	E85985	B91140	E60950	AH0906	S40051	E83061	A60950	S48288	JH0101	AC2737	A97518	AB2103	H86250	T07663	T01266	F69534	B75286	T05350	C64119	B95130	H98000	D97492	AC2710	AG3437
	BB	7	н	~	7	-	~	0	7	7	7	~	ď	7	~	0	~	N	~	7	~	-1	~	~	~	~	N	N	N	0
	Length	965	4563	269	779	309	309	309	275	309	484	412	274	393	784	430	430	493	1025	1230	310	330	332	392	476	477	477	498	498	501
* Query	Match	91.8	91.8	83.7			•	81.6	79.6	79.6	77.6	75.5	71.4	71.4	71.4	69.4	69.4	69.4	69.4	69.4	67.3	67.3	67.3	•	•		67.3	67.3	•	67.3
	Score	45	45	41	41	40	40	40	39					35			34	34	34		33		33					33		33
Result	No.	1	7	m	4	5	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25			28	29

hypothetical prote	starch synthase DU	acetyl-CoA carboxy	acetyl-CoA carboxy	ribosomal protein	salivary glue prot	salivary glue prot	acetyltransferase,	exopolyphosphatase	molybdenum cofacto	probable glycosylt	starch synthase (E	mannonate oxidored	D-mannonate oxidor	fructuronate reduc	cytochrome c-type
AB1875	T01265	T42531	T38906	S78289	S12607	S33822	G87383	AE2652	T46858	B95936	AI0995	E86130	B91289	S56548	E57987
0	0	7	~	~	~	7	~	~	~	~	~	7	0	~	-
680	1674	2279	2280	83	107	112	173	341	394	427	477	486	486	486	552
۳.	e.	۳.	۳.	m.	'n.	'n	'n	۳.	'n.	ĸ.	۳.	m.	m.	m.	m.
67	67.3	67	67	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65	65.3	65	9
		m	33	32	32	32	32	32	32	32	32	32	32	32	32
33	33	n													

## ALIGNMENTS

RESULT 1

S32802
apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C,Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 09-Jul-2004
C,Accession: S32802
R; Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchi
Biochim. Biophys. Acta 1086, 326-334, 1991
A, Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r
A; Reference number: S32802; MUID: 92075708; PMID: 1742325
A;Accession: S32802
A;Status: preliminary
A;Molecule_type: mRNA
A;Residues: 1-596 <pap></pap>
A, Cross-references: UNIPROT: Q28473; EMBL: X15737; NID: 938047; PIDN: CAA33755.1; PID: 99301.
C;Superfamily: apolipoprotein B
Query Match 91.8%; Score 45; DB 2; Length 596;
Hest Local Similarity 90.0%; Fron. No. 0.43; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

### |||||:|||| 226 TRLTRKRGLK 235 1 TRLTRORGLK 10 셤 ò

Apolipoprotein B-100 precursor - human
N; Contains: apolipoprotein B-26; apolipoprotein B-74
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-De-1987 #sequence revision 28-De-1987 #text\_change 09-Jul-2004
C; Date: 28-De-1987 #sequence revision 28-De-1987 #text\_change 09-Jul-2004
C; Date: 28-De-1987 #sequence revision 28-De-1987 #text\_change 09-Jul-2004
C; Date: 28-De-1987 #sequence revision 28-De-1987 #text\_change 09-Jul-2004
C; Date: 28-De-1987 #sequence
R; Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scr
DNA 6, 363-372, 1987
A; Title: DNA sequence of the human apolipoprotein B gene.
A; Reference number: A27850
A; Molecule type: DNA
A; Reseidues 1-617, A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431,'O', 3433-3731, A; Reseidues 1-617, 'A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431,'O', 3433-3731, A; Cross-references: UNIPROT: P04114; UNIPROT: P7842; UNIPROT: P78479; UNIPROT: Qumno; DNA
A; Cross-references: UNIPROT: P04114; UNIPROT: P7842; UNIPROT: P78479; UNIPROT: Qumno; DNA
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: r
A; Reference number: Aj1686
A; MACCESSION: Af1686
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: r
A; Reference number: Aj1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; MACCESSION: Af1686
A; M

A;Molecule type: mRNA A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA> Note: 1109-Agp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

```
R;Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, P.E., Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B CDNA. Evidence for more than on A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Residues: 3846-4298 «SHO»
A;Residues: 3846-4298 «SHO»
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A;Reference number: A25572; MUID:87076044; PMID:3024665
A;Reference number: A25572; MUID:87076044; PMID:3024665
A;Residues: 4219-4337, S', 4339-4563 «PFI»
A;Residues: 4219-4337, S', 4339-4563 «PFI»
A;Cross-references: GS:M36676
B;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T..., Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
A;Recence number: A24738; MUID:86042646; PMID:2932736
A;Accession: A44738; MUID:86042646; PMID:2932736
A;Accession: A44738; MUID:86042646; PMID:2932736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMOIGEUIE type: mRNA
A;Residues: 'N', 3729-3731,'I', 3733-3875,'A', 3877-3948,'F', 3950-3963,'Y', 3965-3982,'S', 391
A;Residues: 'N', 3729-3731,'I', 3733-3875,'A', 2877-3948,'F', 3950-3963,'Y', 3965-3982,'S', 391
A;Chen, S.H., Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cail
Science 238, 363-366, 1987
A;Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
A;Reference number: A40133; MUID:880189; PMID:3659919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Accession: B40133
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: moludes the grop codon of the organ-specific mRNA for apo48
A.Molecule type: protein
A.Molecule type: moludes the grop codon of the organ-specific mRNA for apo48
A.Molecule type: moludes the grop codon of the organ-specific mRNA for apo48
A.Molecule type: moludes the grop codon of the organ-specific mRNA for apo48
B.Hardman, D.A.; protter, A.A.; Schilling, J.W.; Kane, J.P.
A.Molecule type: moluber: A.A.; Schilling, J.W.; Kane, J.P.
A.Molecule type: moluber: Muld: malysis of human B-48 protein confirms the novel mechanism paraces number: A28002; MUID: 88106542; PMID: 3426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: mRNA ARSA ARSA ARSA AREasidues: 2169-2179 4NOS.

A.Reasidues: 2169-2179 4NOS.

A.Reasidues: 2169-2179 4NOS.

A.Note: the sequence shown represents the carboxyl end of apolipoprotein B-48

A.Note: two RNA species 14.1kb and 7.5kb in length, were isolated from the human intest chencodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA, R/Andy. C.7, Kim. T.W.; Wengy, S.1, Lee, B.; Yang, M.; Gotto Jr., A.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990

A.Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A.Reference number: A35783, MUID:90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 28-41,76-97,'I',99-100,175-193,206-215,239-249,259-266,357-399,455-490,512-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stop codon in human intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 3056-3159 <MEH>
A; Residues: 3056-3159 <MEH>
A; Cross-references: GBX.03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
B; Hoppattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in
A; Reference number: A29659; MUID:88049670; PMID:2445342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A29659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aj'Itle: A partial cDNA clone for human apoliprocein B.
A,Reference number: A25774; MUID:85270450; PMID:3860836
A,Receasion. A25774
A,Wolecule type: mRNA
A,Rolecule type: MRNA
                                                                                                                                                                                                A.Molecule type: mRNA
A.Residues: 1-272, 'N',274-617,'A',619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A.Cross-references: GB.XO4506; NID:g34330; PIDN:CAA28191.1; PID:g34331
R;Law, S.W.; Grant, S.M.; Higuntoni, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A;Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A;Reference number: A94134; MUID:87041416; PMID:3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mENA
A; Residues: 1-617, 'A', 619-703,'P',705-792,'R',794-1270,'S',1272-1866,'G',1868-2036,'N',2
4189-4220,'M',422-4563 <LAW>
A; Mole: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M.
J. Biol. Chem. 261, 12918-12921, 1986
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID:87008488; PMID:3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA

A; Residues: 1-97, '1', 99-328, 'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-

9-4132,'(q',4134-4180,'E', 4188-4563 <CHES.

A; Cross-references: GB: J02610; NID: 9178803; PIDN: AAA35549.1; PID: 9178804

A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides

R; Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H

Proc. Natl. Acad. Sci. US.A. 83, 5678-5682, 1986

A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein

A; Reference number: A24320; MUID: 86287319; PMID: 3461454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-97, 1', 99-617, 'A', 619-941, 'YXIWSLPPKP', 951-1138, 'PTGRLPNCFSNGLICYSLWLHSFQE
A; Cross-references: GB:M14081; NID:g1795; PIDN:AAA51752.1; PID:g553189
R; Law, S:W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor, Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A; Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A; Reference number: A24684; MUID:86094221; PMID:3001697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 485-617, 78', 619-1044 < LA2>
A; Residues: 485-617, 78', 619-1044 < LA2>
A; Cross-references: GB: M12480; NID:g178791; PIDN: AAAS1751.1; PID:g178792
B; Proct. A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Kiflitter, Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a CDNA clone encoding the amino-terminal region of human apolipopr A; Reference number: A94088; MUID: 86149325; PMID: 3513177
A;Intle: Complete cDNA and derived protein sequence of human apolipoprotein B-100. A;Reference number: A93639; MUID:87016385; PMID:3763409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA;
Residues: 1-291 cPRO>;
Cross-references: 68-M12681; NID:9178797; PIDN:AAA51753.1; PID:9178798;
Poc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
Troc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
Fittle: A partial cDNA clone for human apoliprotein B.
```

ŌĒ

```
A Accession: JH0102
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-779 < cSMI>
A; Residues: 1-779 < cSMI>
A; Cross-references: UNIPROT: Q60536; GB: M35187
A; Note: this is a revision to the sequence from reference JH0101
B; Smith, T.J.; Hautamaa, D.; Maeda, N.
B; Smith, T.J.; Hautamaa, D.; Maeda, N.
A; Title: Sequence of the putative low-density lipoprotein receptor-binding regions of againg reconnects: annotation
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
                                  apolipoprotein B - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Dapecies: Mesocricetus auratus (golden hamster)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0102
R;Smitch, T.J.
R;Mitch, T.J.
A;Reference number: A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||||:||||
642 SRLTRKRGLK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| ||||||
170 TQLARQRGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: apoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E85985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                A; Molecule type: protein
A; Residues: 873-892, 'K', 894-896 <LE1>
A; Residues: 873-892, 'K', 894-896 <LE1>
A; Residues: 873-892, 'K', 894-896 <LE1>
A; Residues: 873-892, 'K', 894-896 <LE1>
A; Residues: 873-892, 'K', 894-896 <LE1>
A; Rolecule type: protein
A; Residues: 3113, 'L', 3115-3130, 'R', 3132-3133, 'P', 3115-3136, 'R' <LE2>
R; Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.;
J. Biol. Chem. 261, 15364-15367, 1986
A; Title: Structure of the human apolipoprotein B gene.
A; Reference number: Ap2564; MUID: 37751153; PMID: 2946672
A; Contents: annotation; gene structure
R; Wagener, R.; Ffitzner, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 368, 419-425, 1987
A; Title: Studies on the organization of the human apolipoprotein B 100 gene.
A; Reference number: A90715; MUID: 87271140; PMID: 2886136
A; Contents: annotation; pene structure
R; Weisgraber, K.H.; Rall Jr., S.C.
J. Biol. Chem. 262, 11097-11103, 1987
A; Title: Human apolipoprotein B-100 heparin-binding and disulfide bond
A; Reference number: A92665; WUID: 87280197; PMID: 301850
A; Contents: annotation; heparin binding and disulfide bond
R; Dashhi, N.; Lee, D.M.; Mok, T.
Biochem: Biophys. Res. Commun. 137, 493-499, 1986
A; Title: Apolipoprotein B is a calcium binding protein.
A; Reference annotation: A; Reference annotation. Calcium binding protein.
A; Reference annotation. Calcium binding protein.
A; Reference annotation. Calcium binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolypoprotein B-100 - golden hamster (fragment)
C,Species: Mesocricetus auratus (golden hamster)
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C,Accession: C60950
R,Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A;Accession: C60950
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosecule type: DNA
A;Residues: 1-269 < LAM>A;Residues: 1-269 < LAM>A;Residues: 1-269 < LAM>A;Coros-references: UNIPROT:Q60536
C;Superfamily: apolipoprotein B
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
      93
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: annotation; calcium binding R; Carlsson, P.; Wiklund, O.; Bjursell, R; Carlsson, P.; Olofsson, S.O.; Bondjers, G.; Darnfors, C.; Wiklund, O.; Bjursell, Nucleic Acids Res. 13, 8813-8826, 1985
A; Title: Molecular cloning of human apolipoprotein B cDNA.
A; Reference number: 137178; MUID:86093680; PMID:3841204
A; Accession: 137180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.8%; Score 45; DB 1; Length 4563; 90.0%; Pred. No. 2.9; cive 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                A;Title: Human apolipoprotein B: partial amino acid sequence A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.7%; Score 41; DB 2;
80.0%; Pred. No. 1.3;
iive 2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||:|||||
TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||||:||||
216 SRLTRKRGLK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                      A; Accession: A22006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ଧ
```

```
B65112

hypothetical 34.6 kD protein in arcB-gltB intergenic region - Escherichia coli (strain in Special 19.5 specials Escherichia coli (strain in Special Escherichia coli (strain in 10-sep-1998 Escherichia coli (special 10-sep-1999)

C; Datce 10-sep-1999 Escherichia coli Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Eschiol Escherichia coli K-1; Burland, V.; Riley, M.; C. A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Accession: E55112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P45476; GB:AE000400; GB:U00096; NID:g2367203; PIDN:AAC76243
A;Experimental source: strain K-12, substrain MG1655
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-309 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
A,Gene: yhcC
C,Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
  Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 309;
Pred. No. 2.3;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                   ö
Score 41; DB 2;
Pred. No. 3.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
```

RESULT

```
Conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica S. Salmonella enterica subsp. enterica serovar Typhi C.Species: Salmonella enterica subsp. enterica serovar Typhi C.Jocission: Allo been called Salmonella typhi C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C.Accession: AH0906 R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, K.Parkhill, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Aththors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Reference number: AB0502; WUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        starch synthase (EC 2.4.1.21) glgA - Bacillus subtilis
N;Alternate names: starch (bacterial glycogen) synthase glgA
S;Species Bacillus subtilis
C;Date: 19-Mar-1997 #sequence revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 840051; E69632; 836627
R;Kiel, J.A.K.W.; Boels, J.M.; Beldman, G.; Venema, G.
A)OI. Microbiol. 11, 203-218, 1994
A;Title: Glycogen in Bacillus subtilis: molecular characterization of an operon encoding|
A;Reference number: 840048; MUID:94195107; PMID:8145641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Roceule type: DNA
A;Residues: 1-484 <KIES
A;Roceule type: DNA
A;Residues: 1-484 <KIES
A;Roceule type: DNA
A;Residues: 1-484 <KIES
A;Crose-references: UNIPPOT: P393125; EMBL: Z25795; NID: G3397487; PIDN: CAA81043.1; PID: G58081
R;Kunst, F.; Ggasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.; Cho.
A.; Broin, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho.
A.; Brildh, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle!
R;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
T.; Minters, P.; Minter, A.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.;
A;Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Authors: Roshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Atta, Markone, M.; Mréference number: Accepted the Accepted to Number: Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accepted the Name Accept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB15073.1; PID:g2635579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AL513382; PIDN:CAD07846.1; PID:g16504394; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 2;
Pred. No. 3.7;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: STY3508
C;Superfamily: Methanococcus jannaschii conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative ;
                                                      221 TSLTRKRGLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 TRIARERGLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-484 < KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Genetica:
                                                                ద
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cipecies: Escherichia coli
Cipecies: Escherichia coli
Cipecies: Escherichia coli
Cipecies: Becherichia coli
Cipecies: Becherichia coli
Cipecies: Becherichia coli
Cipecies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Cipeciesion: B91140
RiHayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Tile: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Residues: L309 cHAy>
A;Residues: L-309 cHAy>
A;Residues: 1-309 cHAy>
A;Residues: 1-309 cHAy>
A;Residues: L-309 cHAy>
A;Residues: L-309 cHAy>
A;Residues: ECs4090
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-309 <STO>
A;Cross-references: UNIPROT:P45476; GB:AE005174; NID:g12517832; PIDN:AAG58345.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain BDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: dallus gallus (chicken)
C.Species: dallus gallus (chicken)
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision of the apolipoprotein B domain that binds to the LDL A.Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL A.Title: A cross-species comparison of the apolipoprotein B G.Sates and A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A.Title: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Molecule type: mRNA;
|Residues: 1-275 <LAMA;
|Residues: 1-275 <LAMA;
|Residues: 1-275 <LAMA;
|Superfamily: apolipoprocein B
|Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - Bscherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
              A,Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A,Reference number: A85480; MUID:21074935; PMID:11206551
A,Accession: E85985
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.6%; Score 40; DB 2; Length 309;
80.0%; Pred. No. 2.3;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.6%; Score 39; DB 2; Length 275; llarity 80.0%; Pred. No. 3.3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 2
Pred. No. 2.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apolipoprotein B-100 - chicken (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein EC84090 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 TOLARORGIK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 ŤQĽARORĠĽK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

```
probable phosphoprotein phosphatase (EC 3.1.3.16) YBR0921 - yeast (Saccharomyces cereviny NyAlternate names: protein YBR0921; protein YBR125c C;Species Saccharomyces cerevisiae C;Species Saccharomyces cerevisiae C;Species Saccharomyces cerevisiae C;Date: 01-Aug-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004 C;Accession: S48288; S45993; S44703 R;Mannhaupt, G; Stucka, R; Ehnle, S; Vetter, I:; Feldmann, H. Yeast 10, 1363-1381, 1994 A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II. A;Reference number: S48285; MUID:95208357; PMID:7900426 A;Accession: S48288 A;Status; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: DNA
A;Residues: 1-393 <MAN>
A;Cross-references: UNIPROT:P38089; EMBL:X78993; NID:g476045; PIDN:CAA55626.1; PID:g476
R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: 845927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apolipoprotein B-100 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0101; S33128; D60950
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of againet mumber: JH0101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rilaw, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDIA;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: MGI:88052
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residuse: 1-393 <FE2>
A;Croser references: EMBL:Z35994; NID:g536408; PID:g536409; MIPS:YBR125c
C;Genetics:
A;Gene: SGD:PTC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 2R
C;Superfamily: human phosphoprotein phosphatase 1A
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
Local Similarity 77.8%; Pred. No. 29;
es 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:061314; GB:M35186 R;Smith, T.; Hautamaa, D.; Maeda, N. submitted to the EMBL Data Library, May 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Molecule type: mRNA
A, Residues: 427-531,'S',533-700 <LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-531, DNA
A,Cross-references: EMBL:X15191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: SGD:S0000329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       384 TRLERERGL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: $33128
A;Accession: $33128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRORGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: JH0101
A, Molecule type: DNA
A, Residues: 1-784 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: S45993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cipace: 13-Sep-2004
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br. addan, S.J.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.Fitle: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathon, A; Foterence number: A82950; MUID:20437337; PMID:10984043
A; Status: preliminary
A; Residues: 1-412 < < STO>
A; Residues: 1-412 < < STO>
A; Residues: UNIPROT: COHVB8; GB: AECO4882; GB: AECO4091; NID: G9950939; PIDN: AAGO806
C; Genetics: A; Gene: PA4677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claccession: A60950
R.Law, A.; Scott, J.
J.Lipid Res. 31, 1109-1120, 1990
A.ithle: A cross-species comparison of the apolipoprotein B domain that binds to the LDL A.Reference number: A60950; MUID: 90324804; PMID: 2373961
A.Reference number: A60950
A.Residues: 1-274 < LAW>A.Residues: 1-274 < LAWAA.Residues: 1-274 < LA
                                                                      A;Gene: glgA
A;Start codon: TTG
C;Superfamily: starch synthase
C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein PA4677 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein B-100 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%; Score 37; DB 2; Length 412; 87.5%; Pred. No. 12; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.4%; Score 35; DB 2; Length 274; Best Local Similarity 87.5%; Pred. No. 21; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Length 484;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                          77.6%; Score 38; DB 2; 77.8%; Pred. No. 8.9; ative 2; Mismatches
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                            Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.5
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 TRLTKOKGL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 LTRKRGLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRORGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 TKLTRORG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRORG 8
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
```

```
dinydrocrotase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: A20373
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.
Rxarp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, R.; Li, M.; Gordon-Kamm, Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Status: prediminary
A;Status: prediminary
A;Residues: 1-430 «KUR.>
A;Status: prediminary
A;Residues: 1-430 «KUR.>
A;Cross-references: UNIPROT:Q8UFUO; GB:AE008688; PIDN:AAL42313.1; PID:g17739715; GSPDB:C
C;Genetics:
A;Gene: pyrc
A;Gene: pyrc
A;Gene: pyrc
A;Gene: pyrc
C;Genetics:
A;Gene: pyrc
C;Genetics: A;Gene: Acronalar chromosome
C;Superfamily: Bacillus dihydroorctase; Bacillus dihydroorctase homology
                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                             Query Match 71.4%; Score 35; DB 2; Length 784; Best Local Similarity 70.0%; Pred. No. 56; Matches 7; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.4%; Score 34; DB 2; Length 430; Best Local Similarity 66.7%; Pred. No. 51; Matches 6; Conservative 2; Mismatches 1; Indels
F;435-445/Region: receptor binding F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                         :|| |:||||
647 SRLMRKRGLK 656
                                                                                                                                                                                                                            1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLTRQRGLK 10
|: ||||:|
249 RIARQRGVK 257
                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                       ð
```

Search completed: December 29, 2004, 12:39:04 Job time : 10.6591 secs

셤

```
Q7YQR5
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                                                                                                                  028473
                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                      escherichia
shigella fl
shigella fl
                                                                                                                                                                                                                                                                                                                                                                                                         gallus gall
salmonella
salmonella
                                                                                                                                                                                                                                                                                          sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                             glaucomys v
                                                                                                                                                                                                                                                                                                                                         rousettus a
                                                                                                                                                                                                                                                                                                                                                     agouti paca
hydrochoeru
                                                                                                                                                                                                                                                                                                                                                                   erethizon d
                                                                                                                                                                                                                                                                                                                                                                                                                              phalanger o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacillus an
bacillus ce
                                                                                                                                                                                                                                                                            aotus vocif
                                                                                                                                                                                                                                                                                   macaca fasc
                                                                                                                                                                                                                                                                                                                    diceros bic
                                                                                                                                                                                                                                                                                                                            nyctimene a
                                                                                                                                                                                                                                                                                                                                  pteropus hy
                                                                                                                                                                                                                                                                                                                                               chaetophrac
                                                                                                                                                                                                                                                                                                                                                                          mesocricetu
                                                                                                                                                                                                                                                                                                                                                                               mesocricetu
                                                                                                                                                                                                                                                                                                                                                                                                                                     ornithorhyn
                                                                                                                                                                                                                                                                                                                                                                                                                                           tachyglossu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  dinomys bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherurus a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hystrix bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                         rhodopirell
                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                     December 29, 2004, 12:13:11; Search time 58.4091 Seconds (without alignments) 98.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                            OMOU
                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                         013788
P04114
07560
07560
077500
077710
077704
077704
077707
077707
07177
060535
060537
060536
060537
07777
07777
083152
077277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           081k85
081698
                                                                                                                                                                                                                                                                                                                                                                                                                                                       07umf6
07tn65
                                                                                                                                                                                                                                                                             07yqr5
                                                                                                                            1825181
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                           hits satisfying chosen parameters:
                                                                                                               1825181 segs, 575374646 residues
                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                        Q60536
Q60537
YHCC_ECOLI
Q7UBF4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLGA BACAN
GLGA BACCR
                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                          - protein search, using sw model
                                                                                                                                                                                                                                                                                   Q28473
Q13788
APB HUMAN
Q7Z600
                                                                                                                                                                                                                                                                                                                    Q7YR10
Q7YQM8
                                                                                                                                                                                                                                                                                                                                 O7YOM7
O7YR04
O7YR08
O7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                    O7YOM9
O7YON0
                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                   Q7TN72
                                                                                                                                                                                                                                                                                                                                                                                                   283JF2
                                                                                                                                                                                                                                                                                                                                                                                                                28XFV9
                                                                                                                                                                                                                                                                                                                                                                                                                        27CPN5
                                                                                                                                                                                                                                                                                                                                                                                                                              27YQN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27TN69
                                                                                                                                                                                                                                                                                                                                                                                                          271277
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27UMF6
                                                                                                                                                                                       UniProt_02:*
: uniprot_sprot:*
: uniprot_trembl:*
                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                        Query
Match Length DB
                                                                 US-09-823-418-6
49
                                                                              TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                      4445
4445
7480
7480
330
330
330
330
330
330
300
300
300
                                                                                                                                                                                                                                                                                                                    883.7
883.7
883.7
883.7
883.7
883.7
883.7
                                                                                                                             ŏ
                                                                                            Scoring table:
                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                             Fotal number
                          OM protein
                                                                                                                                         Minimum DB
Maximum DB
                                                                               Sequence:
                                                                                                               Searched:
                                                                                                                                                                                        Database
                                        е
0
                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                 Š.
                                       Run
```

```
ö
           Aas43926 bacillus
Aat3448 bacillus
P39125 bacillus en
G6hc18 bacillus th
Q9fxm2 arabidopsis
Q818t0 arabidopsis
Q91va4 arabidopsis
Q91va4 arabidopsis
Q91vb8 pseudomas
Q93915 klebsiella
Q05x28 lactobacill
Q7yqp1 crocuta cro
   9
  272yj6 bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22761261; PubMed=12878460; Amrine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S., Marine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S., Marine-Madgen H., Koepfli K.-P., Wolipoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein B (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB=Liver;
TISSUB=2075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45955 MW; REFA8492157E1BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.81;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 AA
                                                                                                                                                                                                                                                                414 AA
                                                                                                                                                                                                   ALIGNMENTS
072YJ6
AAA33226
AAT34148
CLGA_BACSU
Q6HCTB
Q9PXM2
Q9PXM2
Q9LBTD5
Q9LWA4
Q9LWA6
Q9J915
Q9J915
Q9YQP1
Q9YQP1
Q9YQP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                    Aotus vociferans (Spix's owl monkey).
                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                       Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.8%;
                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
 Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 TRLTRKRGLK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
 NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein.
NON TER
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q28473
Q28473;
```

~

```
SEQUENCE FROM N.A.
MEDLINE=87041416; PubMed=3464946;
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zannis V.
             OC STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE STATES TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APB_HUMAN STANDARD, PRT, 4563 AA. P00114; 00052; Q13787; 01.00V-1986 (Rel. 03, Created) 01-N0V-1986 (Rel. 03, Last sequence update) 05-70JL-2004 (Rel. 44, Last annotation update) MpOilpoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: Apolipoprotein B-100] [Contains: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-87191999; PubMed=2883086;
Carlseon P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure the B.74 region.";
Gene 49:29-51(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
metabolism in the cynomolgus monkey: evidence for post-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 2; Length 3262;
Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                            Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56603BC0618DD40D CRC64;
                                                                                                                                                                                                                                                                                                      596 596
596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; MIS421; AAAS1758.1; -.
PIR; A27850; LPHUB.
GO; GO:00005576; Cextracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
GO; GO:0006869; P:lipid transport; NAS.
                                                                                                                                                                                                                                                                                                                                                                                    Match
Local Similarity 90.0%; Pred. No. 1.2;
de 9; Conservative 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 3262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                          transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3262 AA; 370140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       013788,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.8%;
90.0%;
                                                                                                                                                                                                       EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                            TISSUE=Liver;
Murray R.;
Submitted (FEB-1992) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 TRLTRKRGLK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APOB protein (Fragment)
Name=APOB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=9606;
                                                                                                                                                                                                                                                           Lipoprotein.
NON TER
                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=APOB;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     013788
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APB HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSSEDITATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
B-100: relationship between apoB-100 and apoB-48 forms.";
EMBO J. 5:3495-3507(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE=87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahley R. M., Scott J.; "Mathey R. M., Scott J.; Mathey R. M., Scott J.; "Human apolipoprotein B: structure of carboxyl-terminal domains, sites of gene expression, and chromosomal localization."; Science 230:37-43(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 3109-4563 FROM N.A.
MEDLINE=88300528; PubMed=2994225;
KRott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priserley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 3056-3159 FROM N.A.
MEDLINE=66641888; PubMed=3903660;
Mehrabian M., Schumaker V.N., Farred G.C., West R., Johnson D.F.,
Kirchgesener T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and characterization of RRNA.";
                                                                                                                                            MEDLINE-87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE-88003974; PubMed=352907;
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J., Lee N., Brewer H.B. Jr., "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-86093680; PubMed=3841204;
Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
Bjursell G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87161758; PubMed=3030729;
Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of human apolipoprotein B cDNA.";
Nucleic Acids Res. 13:8813-8826(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 709-906 FROM N.A.
MEDILINE-B8270450; PubMed=3860836;
Deeb S.S., Motulsky A.G., Albers J.J.;
"A partial cDNA clone for human apolipoprotein B
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derived amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986)
                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 14:7501-7503 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 261:12918-12921(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 13:6937-6953 (1985)
```

m

```
VARIANT LEU-2739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7Z600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 072600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
Q7Z600
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                       Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V., Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.; "Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L., "Sequence, receptor-binding domains and internal repeats of human apolipoprotein B-100.", Nature 323:738-742(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100.";
Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                귱
                                                                                                                                                                                                          MEDIINE-88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cai S.-J., Dealypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.;
"Apolipoproctein B-48 is the product of a messenger RNA with an organ-
specific in-frame stop codon.";
Science 238:363-366(1987).
                                                                                                                                                                                                                                                                                                                                                                                                           "Complete protein sequence and identification of structural domains human apolipoprotein B."; Nature 323:734-738(1986).
                                                                                         [11]
SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE-86287319; PubMed=3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of cDNA clones encoding the entire B-26 region of human
                                                                                                                                                                                                                                                                                                                                                         Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr., Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R., Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91071750; PubMed=1979313;
Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Rozlese G., Tanglein F., Rozlese G., "Betection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89098975; PubMed=2563166;
Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.;
"Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and triglycerides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprotein B is a calcium binding protein.";
Blochem. Blophye. Res. Commun. 137.493-499(1986).
                                                                apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                      apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20143590; PubMed=10679026;
                                                                                                                                                                                                                                                                                                                                                MEDLINE=87039351; PubMed=3773997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Cell 11:721-734(2000).
               MEDLINE=86149325; PubMed=3513177;
 SEQUENCE OF 1-291 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALMITOYLATION OF CYS-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genet. 86:91-93 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALCIUM-BINDING DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT FDB GLN-3527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT SER-4338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAINS.
                                                                                                                                                                                                                                                                                                                                   DOMAINS.
```

```
FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                       MEDINE=95190020; PubMed=7883971;
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
Hennilial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS SER-1914, ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432 AND ILE-3921.
MEDLINE-9811125; PubMed=9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97044521; PubMed=8889592;
Doriter O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
MEDLINE-91016974; PubMed-2216805; Manag L.-S., Gavish D., Breslow J.L.; "Hanag L.-S., Gavish D., Breslow J.L.; "Sequence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabes J.P., Varret M., Saint-Joré B., Erlich D., Jondeau G., Krempf M., Glraudet P., Junien C., Bolleau C.; Familial ligand-defective apolipoprotein B-100: simultaneous detection of the ARG3500-->GLN and ARG3531-->CYS mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1; Length 4563; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C., Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Apolipoprotein B (Including Ag(X) antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS FDB GLN-3527 AND CYS-3558.
MEDLINE=97403938; PubMed=9259199;
                                                                                                                                                                                                                                                                                                                                                                 Clin. Invest. 95:1225-1234(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR-SSCP.";
Hum. Mutat. 8:282-285(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 102:44-49(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypocholesterolemia.".
Hum. Genet. 102:44-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND THR-4481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            population.
Hum. Mutat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=APOB;
```

ö

```
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AYZ43375; AAP50763.1; -.
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                Apolipoprotein B 100 (Fragment).
                                                                                83.7%;
80.0%;
                                                                    Query Match
Best Local Similarity 80...
8; Conservative
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 80.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                          275 SRLTRKRGLK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||||:||||
279 SRLTRKRGLK 288
                                                                                                                        1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                          436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pteropodinae; Pteropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLTRORGLK 10
                                     1
432 4
432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              1
436 4
436 AA;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=48988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9405;
                             Lipoprotein.
NON TER
NON TER
SEQUENCE 43
                                                                                                                                                                                                                                                        Name=apoB-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                            Q7YOMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7YQM7
                                                                                                                                                                       RESULT 8
Q7YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7YQM7
         Z K Z F F S
                                                                                                                       ð
                                                                                                                                        셤
                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
4polipoprotein B (Fragment)
6laucomys volans (Southern flying squirrel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An ewe phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Perissodactyla, Rhinocerotidae, Diceros.
NCBI_TaxID=9805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-22761261; PubMed=12878460;
MEDLINE-22761261. K.-P., Wayne R.K., Springer M.S.,
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.,
"A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                   Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2; Length 421;
Pred. No. 5.8;
2; Mismatches 0; Indels
                                                                                                                                        0; Indels
                                                                                           4563 AA; S15553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          46747 MW; D47B77BD4F864FD1 CRC64;
01-0cr-2003 (TrEMBLrel. 25, Created)
01-0cr-2003 (TrEMBLrel. 25, Last sequence update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Diceros bicornis (Black rhinoceros).
                                                                                                                 Score 45; DB 2;
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                  421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 AA.
                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                 91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.7%;
80.0%;
                                                                                                                                      9; Conservative
                                                                                                                                                                    |||||:||||
3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :[|||:||||
264 SRLTRKRGLK 273
                                                                                                                                                        1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRQRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AA;
                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=64683;
                                                                                   Lipoprotein.
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                        Glaucomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                        Q7TN68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7YR10;
                                                                                                                                                                                                                            Q7TN68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7YR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7YR10
  ð
                                                                                                                                                                          셤
                                                                                                                                                                                                                                        à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Nyctimene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22761261; PubMed=12878460; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; An bwe phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships "; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22761261; PubMed=12878460; Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.; Antine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.; "A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pteropus hypomelanus (Small flying fox).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Chiroptera, Megachiroptera, Pteropodidae,
                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                          Score 41; DB 2; Length 432;
Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.7%; Score 41; DB 2; Length 436;
80.0%; Pred. No. 6.1;
iive 2; Mismatches 0; Indels
432
48171 MW; F27B7AB39604732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48717 MW; 1C4A7EAD72D2C629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nyctimene albiventer (Common tube-nosed fruit bat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-077-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 AA
                                                                                                                                                                    2; Mismatches
```

ö

Gapa

ö

445 AA

```
MEDLINE=22761261; PubMed=12878460;
Marine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; MY2431369; AAPS0757-1;
InterPro: IPR000871; Beta lactanase A.
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                           Agouti paca (Paca).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
NCBI_TaxID=108852;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An by Dylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Hydrochaeridae,
                           83.7%; Score 41; DB 2; Length 445; 80.0%; Pred. No. 6.2; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.7%; Score 41; DB 2; Length 445; 80.0%; Pred. No. 6.2; Live 2; Mismatches 0; Indels
445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrochoerus hydrochaeris (Capybara) (Carpincho).
                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25,
          Query Match
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 80.(
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 SRLTRKRGLK 297
                                                                                   1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 445
                                                                                                                                                                                                                                                                                Name=apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
NON TER
NON TER 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein.
NON TER
NON TER
SEQUENCE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrochaerie
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07TN71;
                                                                                                                                                                                         Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                           27TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7TN71
                                                                                                               셤
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22761261; PubMed=12878460; MEDLINE=22761261; PubMed=12878460; Amrine-Madgen H., Koepfil K.-P., Wayne R.K., Springer M.S.; Amrine-Madgen H., Koepfil K.-P., Wayne R.K., Springer Compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                 Rousettus amplexicaudatus (Common rousette).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Rousettus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-2761261. PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243378; AAPS0766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chaerophractus villosus (South American armadillo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Edentata, Dasypodidae, Chaetophractus.
                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                83.7%; Score 41; DB 2; Length 438;
80.0%; Pred. No. 6.1;
tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.7%; Score 41; DB 2; Length 438;
80.0%; Pred. No. 6.1;
1ive 2; Mismatches 0; Indels
                                                        48734 MW; 2BD85BCBF4E2CC41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48597 MW; 41C890DEAF95C872 CRC64;
                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                   438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 AA.
                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
EMBL; AF548436; AAP97392.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Gest Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                       Apolipoprotein B (Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apolipoprotein B (Fragment
                                                                               Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                            :|||:||||
281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||||:||||
281 SRLTRKRGLK 290
                            1
438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
445
                                                                                                                                             1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTRORGLK 10
                           1
438 4
438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=29080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipoprotein.
NON_TER
NON_TER 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein.
NON TER
NON TER
SEQUENCE 43
             Lipoprotein.
NON TER
                           NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7YR08
                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                    Q7YR04
                                                                                                                                             ઠે
                                                                                                                                                                        g
                                                                                                                                                                                                                                                                 ଚ
```

ö

Gaps

ö

445 AA

```
ò
                                                                                  g
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGUENCE FROM N.A.

MEDLINE=90236377; PubMed=2332175;

MEDLINE=90236377; PubMed=2332175;

A Smith T.J., Hautamaa D., Maeda N.;

"Sequence of the putative low-density lipoprotein receptor-binding T regions of apolipoprotein B in mouse and hamster.";

T regions of apolipoprotein B in mouse and hamster.";

R PIS, 310(1990).

R PIR, J06050; C60950.

M Lipoprotein.

I Lipoprotein.

I NON TER 780 780

SEQÜENCE 780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-22761261; PubMed=12878460;
MEDLINE-22761261; Verbfill K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Wol. Phylogenet. Evol. 28:225-240(2003).
EMBL; Ar243368; AAP50756.1; -.
                                                                                                                                                                                                                                                        Erethizon dorratum (North American porcupine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Erethizontidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleogtomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
Query Match 83.7%; Score 41; DB 2; Length 445; Best Local Similarity 80.0%; Pred. No. 6.2; Matches 8; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0%; Pred. No. 6.2;
Matches 8; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 AA; 49617 MW; 9572FE5F5E7625F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 780 780 780 780 780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEWBLrel. 01, Created)
01-NOV-1996 (TrEWBLrel. 01, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Hamster apolipoprotein (apoB) (Fragment).
Mesocricetus auratus (Golden hamster).
                                                                                                                                                                       445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    780 AA
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                               :||||:||||
288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=34844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
NON TER
SEQUENCE
                                                                                                                                                                                    07TN72
                                                                                                                                                                   Q7TN72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 965090
                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                 ò
                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
Query Match
83.7%; Score 41; DB 2; Length 780;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TRLTRQRGLK 10
Db 642 SRLTRKRQLK 651
```

Search completed: December 29, 2004, 12:37:33 Job time : 59.5202 sece

```
December 29, 2004, 12:10:41; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                        2002273
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                               2002273 segs, 358729299 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Geneseq 23Sep04:*

1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003as:*
                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                   US-09-823-418-7
                                                                                                                                                                                                                      TRLTEKRGLK 10
             Copyright
                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                           Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Aay30688 Apo-BIOO Aay30689 Apo-BIOO Aaw57205 Apo B bin Aaw57207 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw56845 Nucleic a Aaw66845 Nucleic a Abb77687 Peptide # Abg52504 Human apo Aaw56845 Nucleic a Abb77687 Peptide # Abg52504 Human apo Aaw41262 Apolipopr Aar14031 Sequence Aar1227 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Aav11237 Human apo Description AAY30689 AAW57205 AAW41261 AAW96892 ABU37575 ABU37575 ABU37575 ABU37576 AAW57209 AAW57209 AAW96845 B Query Match Length Result No.

Z E X X X X X X X X X X X X X X X X X X	The proceeding the proceeding to the proceeding the proceeding that proceeding the atherosclerosis.  XX atherosclerosis.  Py atherosclerosis.  XX Claim 17; Page 57; 70pp; English.  CC AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which compulate atherosclerosis. The peptides are derived from amino acids 3358 CC to 3367 of aposl100. The method comprises detecting compounds which affect come be used for identifying compounds with proteoglycan (PG). The method comprises detecting compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent catherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the cutdy of atherosclerosis, and in vivo assay methods for identifying
ဥ	compounds which modulate atherosclerosis and/or LDL-PG binding. They can

ABB37687 ABG52504 AAR72704 AAR34031 ADJ57400 AAY31237 AAW41262

AAW96826 AAU98981 ADD48677 AA015893 ABR40253

377 2463 3923 44536 4550 4560 4563 4563

## ALIGNMENTS

Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Ą. AAY30688 standard; peptide; 10 98US-0077618P. 99WO-US004805 (first entry) (REGC ) UNIV CALIFORNIA. Synthetic. Homo sapiens. WO9946598-A1 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999 AAY30688; RESULT 1

Boren JOS; Innerarity TL,

WPI; 1999-551509/46.

identifying compounds which affect binding of low density lipoprotein

ö

Сарв

ö

Length 10; 0; Indels

Score 46; DB 2; Pred. No. 0.027; 1; Mismatches

93.9%; 90.0%;

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

Sequence 10 AA;

S

1 TRLTEKRGLK 10 |||||:||||| TRLTDKRGLK 10

us-09-823-418-7.rag

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which mather selectorists. The peptides are derived from amino acids 3358 to 3357 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which proteoglycan (FG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to atherosclerosis. The transpending one that compounds which medual and prevent express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which reculs and in vivo assay methods for identify can be used to determine whether also be used to identify compounds which result in an increase in also be used to a particular food or drug composition tends to stimulate or inhibit the used in gene thersey for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 57; 70pp; English.
identify
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                    1 TRLTEKRGLK 10
                                                                                                                                                                                                           1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4PI; 1999-551509/46.
                                                                                                                                     Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atherosclerosis.
                                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innerarity TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                        17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                            AAY30689;
                                                                                                                            Query Match
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                   RESULT 2
 8888888
                                                                                                                                                                                                           유
                                                                                                                                                                                    8
```

ô also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing Gaps Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. ; 0 100.0%; Score 49; DB 2; Length 10; 100.0%; Pred. No. 0.0067; tive 0; Mismatches 0; Indels AAY30689 standard, peptide, 10 AA. 99WO-US004805 98US-0077618P (first entry) Boren JOS;

Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.

Apo B binding site peptide 2.

03-AUG-1998 (first entry)

AAW57205;

Ä

AAW57205 standard; peptide; 11

RESULT 3

셤 8

The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Nonnaturally occurring, receptor-competent LDL particles are useful as: (1) carg-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Nonnaturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor ö Gaps ö 89.8%; Score 44; DB 2; Length 11; 90.0%; Pred. No. 0.074; 1.1ve 0; Mismatches 1; Indels Conservative 1 TRLTEKRGLK 10 Similarity Sequence 11 AA; • Query Match Best Local 8 Best Loc Matches ð 셤

11

TRLTRKRGLK

Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.

Claim 12; Page 52; 73pp; English.

ö

Baillie

Halbert GW, Owens MD,

WPI; 1998-230637/20.

(UYST ) UNIV STRATHCLYDE.

97WO-GB002610. 96GB-00020153.

25-SEP-1997; 27-SEP-1996;

02-APR-1998

WO9813385-A2

Synthetic.

Synthetic

AAW57207;

```
This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKHRHS-X2-T-Z2 (I) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (a); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 cc a. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated containing or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits which is active as such or as part of a 98-aa peptide, inhibits cativation of the prothrombinase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                      Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 2; Length 15;
Pred. No. 0.1;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UNIO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW96892 standard; peptide; 15 AA.
                                                            Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                             97WO-GB001255
                                                                                                                                                                                                                                                                                                                                                                                                                          96GB-00009702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ettelaie C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.06
                  19-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                     anglogenesis; cellular prothrombinase complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1996;
                                                                                                                                                                                                                                                                                     WO9743311-A1
                                                                                                                                                                                                                                                                                                                                 20-NOV-1997.
                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
AAW96892
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-caturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least leptide component that has at least 1 binding site for an apo B protein creceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKKNKHRH (1) or TTRLTRKRGLK (2), or their connect Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles are apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                      Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 2; Length 13;
Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "attached to retinoic acid"
                                                                                                                                                                                               Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                            AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW41261 standard, peptide, 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baillie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-00020153
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TRLTRKRGLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTEKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9813385-A2
                                                                                                                                                  03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halbert GW,
```

ö

Gaps

;

Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;

AAW41261

RESULT 5 AAW41261

요 ઠ

Matches

us-09-823-418-7.rag

20-JUL-2001; 2001US-0306726P

```
ò
                                                                                                                                                                                                                                                                                                                                                                  셤
apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;
nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;
non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                       AAM96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VDD), intermediate density present sequence can be used in the composition of the invention. The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic calls, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                         Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                  Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                     (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ37575 standard; peptide; 20
                                                                                                                                       97US-00874807.
98US-00079030.
                                                                                                                  98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                           cancers (particularly non-sma
fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-2002, 2002WO-US023419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rkirkkeik 15
                                                                                                                                                                                                                   WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003007689-A2.
                                                                                                                10-JUN-1998;
                                                Homo sapiens
                                                                                                                                                   14-MAY-1998;
                                                                   WO9856938-A1
                                                                                                                                      13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentifled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2003
                                                                                                                                                                                                                                                                  treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ37575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                      6; Length 20;
                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                   Score 44; DB 6;
Pred. No. 0.14;
0; Mismatches
                                             Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW57208 standard; peptide; 22 AA.
                                                                                                                                                      Disclosure, Fig 2, 79pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baillie G;
                                                                                                                                                                                                                                                                                                                                                              .
0
                                      Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                             retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owens MD,
                                                                    WPI; 2003-300420/29.
ETH ZUERICH
UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                 7 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                    Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW57208;
                                                                                                                                                                                                                                                                                                                              Query Match
(ETHZ-)
             (OXZO-)
                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
```

```
site peptide analogue which can be used as a component of a non-
aturally occurring, receptor-competent low density lipoprotein (LDL)
particle of the present invention. The LDL particle comprises at least 1
peptide component that has at least 1 binding site for an apo B protein
receptor and at least 1 lipophilic substituent. Also described in the
invention are peptides containing an apo B binding sequence with a least
70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their
dimers. Non-naturally occurring, receptor-competent LDL particles are
useful as: (1) drug-targeting vectors for delivering anticancer drugs to
cancer cells that express an apo B protein receptor, and (ii) additives
                                                                                                                                                                                                                                                                                                                                                                                                         for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                     sequence represents a specifically claimed Apo B 100 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     affinity to an apo B protein receptor
                           Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22 AA;
```

89.8%; Score 44; DB 2; Length 22; 1; Indels Pred. No. 0.15 0; Mismatches 90.06; Conservative 1 TRLTEKRGLK 10 16 TRLTRKRGLK Best Local Similarity Matches 9; Conserv Query Match 8 硆

ö

Gaps ;

> Apo B 100 binding site peptide analogue peptide D. AAW57209 standard; peptide; 22 (first entry) 03-AUG-1998 AAW57209; AAW57209 RESULT

Ź

Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site. /note= "attached to retinoic acid" Location/Qualifiers Key Modified-site Synthetic

WO9813385-A2

02-APR-1998

97WO-GB002610. 25-SEP-1997;

96GB-00020153 27-SEP-1996;

STRATHCLYDE UNINO ( TSYU) Baillie G; Owens MD, Halbert GW,

WPI; 1998-230637/20.

The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) peptide binding to apo B protein delivering drugs to cancer cells Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor. Claim 13; Fig 7; 73pp; English.

```
ö
particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDE), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDE. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDE. In a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                    Score 44; DB 2; Length 22;
Pred. No. 0.15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE14541 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                        89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yla-Herttuala S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ARKT-) ARK THERAPEUTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                         Local Similarity 90.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                          TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-179777/23.
                                                                                                                                                                                                                                                                 Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200206314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Narvanen O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide p62
                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE14541;
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE14541
        셤
                                                                                                                                                                                                                                                                                                                                                                                       8
```

```
Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.
                                                                                                                                                                                                                         hypercysteinaemia; factor VII; cardiovascular disease; pathogén; virus.
                                                                                                                                                                                Factor V, human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion;
                                                                                                                                                         Human apolipoprotein peptide fragment #1.
                                                                           AAW64587 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                  Moritz B, Kiessig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-416142/36.
                                                                                                                                                                                                                                                                                                                                                                                        (IMMO ) IMMUNO AG.
                                                                                                                                 23-OCT-1998
                                                                                                                                                                                                                                                     Homo sapiens,
                                                                                                                                                                                                                                                                                                                                   12-JAN-1998;
                                                                                                                                                                                                                                                                                                        12-AUG-1998.
                                                                                                                                                                                                                                                                               EP857973-A2.
                                                                                                      AAW64587;
                                                              AAW64587
                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                        Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                    Gaps
                                                                                                    ö
                                                                                                                                                                                                                                                                                              Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                       Length 34;
                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.8%; Score 44; DB 2; Length 36; 90.0%; Pred. No. 0.25; 1; Indels :ive 0; Mismatches 1; Indels
                                                                     Score 44; DB 5;
Pred. No. 0.24;
                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore JP;
                                                                                                                                                                                                               AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16, Fig 12C; 293pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                     89.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00874807.
98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoogeveen RC,
                                                     Query Match
Best Local Similarity 90.00
Best Local 9; Conservative
                                                                                                                                                                                                                                                                     22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                       1 TRLTEKRGLK 10
                                                                                                                                               25 TRLTRKRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-070331/06.
                                         Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guevara JG,
                                                                                                                                                                                                                                             AAW96876;
                                                                                                                                                                                                                               ន្តដ្ឋប្រ
                                                                                                                       à
                                                                                                                                               셤
```

Schenk V;

Lang H,

98EP-00890007.

(first entry)

TRLTRKRGLK 20

11

```
AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the used with Factor V protein fragments in a novel method to detect the presence of a mutated protein. In a sample that may also contain the corresponding wild type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain alleles of apoß indicates increased risk of developing Alzheimer's calseles of apoß indicates increased risk of developing Alzheimer's (associated with hypercysteinaemia and venous thrombosis) and factor VII mutations (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method does not require complex apparatus for polymerase chain reactions, it is simple, standardisable and reliable and is sample to be quantified

"Second Particularly suited to routine screening. It also allows mutant protein to be applied to the protein or the particularly suited to routine screening. It also allows mutant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 2; Length 37;
Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW96845 standard; peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Query Match
Beet Local Similarity 90.u,
Beet Local Similarity 90.u,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TRLTRKGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
AAW96845
ID AAW96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

ö

Gaps

ô

1; Indels

1 TRLTEKRGLK 10

```
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, liver, cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%; Score 44; DB 4; Length 343; 90.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 31152.
                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG52504 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033346.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00234289.
                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                             04-OCT-2000; 2000GB-00024263.
                                                                                                                                          26-MAY-2000; 2000US-0207456P.
30-UIN-2000; 2000US-00603408.
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                             30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 TRLTRKRGLK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 343 AA;
WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ношо варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG52504;
                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (IDL), low density lipoproteins ((LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic calls, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                     Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinom; diabetes; arteriosclexosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96827-77 represent nucleic acid binding domains derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #5193 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.8%; Score 44; DB 2; Length 51; 90.0%; Pred. No. 0.36; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                 Nucleic acid binding domain from apoB-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 151; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB37687 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                      98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                            97US-00874807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hoogeveen RC,
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||| |||||
TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-070331/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51 AA;
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                    WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                   10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                          22-APR-1999
                                                                                                                                                                                                                                                                                                                          17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment.
                 AAW96845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB37687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB37687
```

ઠે

ö

Gaps

ö

1; Indels

(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR, Hanzel DK, Penn SG,

WPI; 2001-488898/53

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

Claim 27; SEQ ID NO 31152; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipporteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published\_pot\_sequences 

Sequence 343 AA;

Gaps ö Query Match

89.8%; Score 44; DB 4; Length 343;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels

ô

1 TRLTEKRGLK 10 ò 셤

Search completed: December 29, 2004, 12:28:49 Job time : 61.0227 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-7 49 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 TRLTEKRGLK 10 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

,		dp				
Result No.	Score	Query Match	Length	DB	ID	Description
	44	89.8	596	5	S32802	apolipoprotein B -
7	44	89.8	4563	-	LPHUB	apolipoprotein B-1
m	40	81.6		~	C60950	apolipoprotein B-1
4	40	81.6	779	~	JH0102	apolipoprotein B -
τυ.	38	77.6	275	7	E60950	apolipoprotein B-1
9	36	73.5	406	N	AI0767	probable glycosylt
7	36	73.5	406	~	A90985	hypothetical prote
80	36	73.5	406	~	D85830	
o,	36	73.5	406	~	C64970	_
10	36	73.5	407	~	S52148	
11	36	73.5	411	~	S15296	hypothetical prote
12	35	71.4	313	~	E69580	endo
13	35	71.4	461	~	S72953	probable GTP-bindi
14	35	71.4	462	N	F87080	probable GTP-bindi
15	34	69.4		7	T41529	hypothetical prote
16	34	69.4		~	E82104	
17	34	69.4		~	T01873	hypothetical prote
	34	69.4		~	A60950	apolipoprotein B-1
19	34	69.4		N	AG1306	D-alanyl-D-alanine
20	34	69.4		~	C64119	starch synthase (E
21	34	69.4	784	~	JH0101	apolipoprotein B-1
22	34	69.4	1073	~	T01955	hypothetical prote
23	34	69.4	1241	~	H84486	probable helicase
24	34	69.4	1265	~	F84517	probable helicase
25	34	69.4		~	D86481	189.6K hypothetica
	34	69.4	-	N	T48965	hypothetical prote
27	33	67.3	210	N	140540	varD protein - Pse
28	33	67.3	231	~	AF0336	aspartate racemase
29	33	67.3	309	7	AH0906	conserved hypothet

PBSX prophage ORF	protein F28J9.3 [i	starch synthase (E	protein F28J9.6 [i	hypothetical prote	hypothetical prote	DNA ligase (NAD) (	apolipoprotein B -	gene 50 protein -	uncharacterized co	50S ribosomal prot	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical_prote	dipicolinate synth
H69732	F86486	S40051	C86486	E71008	T05129	A40363	865460	ZTBPT9	E97335	E90018	B64440	H70665	D82392	T27458	C83950
N	~	~	~	N	~	N	~	Н	N	~	-	~	N	7	~
325	436	484	490	493	559	9/9	1058	125	143	145	205	225	277	285	292
ო.	'n	۳.	ų	r.	'n	m.	ų	۳.	'n	۳.	'n	'n	65.3	m.	ų.
	67	67	67	67	63	67.3	67	65	65	65	65	65	65	65	65
6									۰.	Δ1					٥,
33 67	33	33	33	33	33	33	33	32	3	Ä	32	32	33	32	37

#### ALIGNMENTS

```
apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S2802
R;Pape, M.E.; Caselle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchir Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: S32802
A;Accession: S32802
A;Accession: S32802
A;Accession: S32802
                                                                                                                                                                                                                                                                                                                           A;Molecule_type: mRNA
A;Residues: 1-596 cPAP-
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301
C;Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2;
Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
```

# 226 TRLTRKRGLK 235 셤

1 TRLTEKRGLK 10

ò

Deficies: Be-100 precursor - human
N; Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
N; Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C; Species: Homo sapiens (man)
C; Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C; Accession: A27850; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A2.
A; Accession: A27850; A2874; I39469; I84624; I37179; PS0568
R; Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scr.
DNA 6, 363-372, 1987
A; Title: DNA sequence of the human apolipoprotein B gene.
A; Reference number: A27850; MUID:88003974; PMID:3652907
A; References: Loss of the human apolipoprotein B gene.
A; Residuae: 1-61,'A', (19-1929,'F', 1931-3318,'D', 3320-3426,'T', 3428-3431,'Q', 3433-3731,'A; Residuae: 1-61,'A', (19-1929,'F', 1931-3318,'D', 3320-3426,'T', 3428-3431,'Q', 3433-3731,'A; Residuae: 1-61,'A', (19-1929,'F', 1931-3318,'D', 3320-3426,'T', 3428-3431,'Q', 3433-3731,'A; Cross-references: UNIPROT:P04114; UNIPROT:P7482; UNIPROT:P78479; UNIPROT:Q9UMNO; UNIPROT: P78-3507, 1986
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: r
A; Reference number: A91058; MUID:87161758; PMID:3030729
A; Accession: A25679

A;Molecule type: mRNA A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA> A;Note: 1109-Agp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

```
Accession: A29659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A.241.

A; Accession: A.241.

A; Accession: A.241.

A; Accession: A.241.

A; Residues: 1-291.

A; Residues: 1-291.

B; Deab, S.S.; Motulsky, A.G.; Albers, J.J.

B; Deab, S.S.; Motulsky, A.G.; Albers, J.J.

B; Deab, S.S.; Motulsky, A.G.; Albers, J.J.

B; Deab, S.S.; Motulsky, A.G.; Albers, J.J.

B; Deab, S.S.; Motulsky, A.G.; Albers, J.J.

B; Deab, S.S.; Motulsky, A.G.; Albers, J.J.

B; Deab, S.S.; Motulsky, A.G.; Albers, J.J.

A; Reference number: A25774; MulD: 98270450; PMID:3860836

A; Residues: 709-791, SSSWKAASHGCPHSAGD', 810-906 < DEE>

A; Residues: 709-791, SSSWKAASHGCPHSAGD', 810-906 < DEE>

A; Residues: 709-791, SSSWKAASHGCPHSAGD', 810-906 < DEE>

A; Residues: 709-791, SSSWKAASHGCPHSAGD', 810-906 < DEE>

A; Carlsson, P.; Darnfors, C.; Oldsson, S.O.; Bjursell, G.

A; Title: Analysis of the human apolipoprotein B gene; complete structure of the B-74 reg

A; Reference number: A1565; MulD: 97191999; PMID:2883086

A; Residues: 1282-2721, 2742-3290, L', 3292-3336, N', 3338-3948, F', 3950-3963, Y', 3965-4180,

A; Residues: 1282-2721, C742-3290, L', 7292-3336, N', 3338-3948, F', 3950-3963, Y', 3965-4180,

A; Residues: 1282-2721, C742-3290, L', 7292-3336, N', 338-3948, F', 3950-3963, Y', 3965-4180,

A; Reference number: A2671, MulD:88058032; PMID:3676265

A; Reference number: A2671, MulD:88058032; PMID:3676265

A; Residues: 1671-2323, 'PYW', 2227-2352, 'H', 2354-2398 < HAR>
A; Residues: 1671-2323, 'PYW', 2217-2352, 'H', 2354-2398 < HAR>
A; Residues: 1671-2323, 'PYW', 2107-2352, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H', 2100-2323, 'H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: mRNA

A, Residues: 1-97, I', 99-328, 'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-
4132,'G',4134-4180,'E',4182-4563 -CHES

A, Cross-references: GB.J02610, NID: 9178803; PIDN: AAA35549.1; PID: 9178804

A, Note: a total of 236 residues were confirmed by direct sequencing of tryptic peptides
R, Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H
Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986

A; Fitle: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
A; Recence number: A24320; MUD: 86287319; PMID: 3461454
A; Recension: A2430; MUD: 86287319; PMID: 3461454
A; Residues: I-97,'I', 99-617,'A', 619-941,'YYIWSLPPKP', 951-1138,'PTGRLPNCFSNGLICYSLWLHSFQE
A; Read Sci. U.S.A. 82, 8340-8344, 1985
B; Law, S.W.; Lackner, K.J.; Hospettankar, AV.; Anchors, J.W.; Sakaguchi, A.Y.; Naylor,
A; Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A; Reference number: A24684; MUID: 86094221; PMID: 3001697
                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'
A; Residues: 1-272, 'N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679, 'Q'
A; Cross-references: GB:XX04506; NID:934331
B; Law, S.W.; Grant, S.W.; Higouchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID:87041416; PMID:3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-617, A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
4189-4220, 'M', 4222-4563 < LAW>
A; Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID: 87008488; PMID: 3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA, A; 619-1044 <LA2>
A; Residues: 485-617, A; (19-1044 <LA2>
A; Cross-references: GB; MI2480; NID: 8189111119; J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki Proct. Natl. Acad. Sci. US: A; 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolitopic A; Reference number: A94088; MUID: 86149325; PMID: 3513177
A; Accession: A23817
A; Residues: 1-291 <PRO>
A; Residues: 1-291 <PRO>
                                human apolipoprotein B-100,
A,Title: Complete cDNA and derived protein sequence of PA,Reference number: A93639; MUID:87016385; PMID:3763409 A,Accession: A25263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A25267
```

```
Rishoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.; Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Residues type: mRNA
A;Residues: 3846-4298
A;Residues: 3846-4298
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A;Title: Isolation, expression and characterization of a human apolipoprotein B 100-speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: A25572
A, Accession: A25572
A, Accession: A25572
A, Accession: A25572
A, Accession: A25572
A, Accession: A25572
A, Accession: A2573
A, Cross-references: GB M3676
A, Accession: A219-4337, S, 4339-4563 < PFI>
A, Cross-references: GB M3676
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, Accession: A24738
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A2474
A, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 2165-2179 <CH1>
A; Residues: 2165-2179 <CH1>
A; Accession: argusts)
A; Residues: 2165-2179 <CH1>
A; Cross-references: GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:g178800
A; Cross-references: GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:g178800
A; Residues: 51-75; D10-110; D29-139; D39-139;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŌF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 2169-2179
A; Molecule type: mRNA
A; Residues: 2169-2179
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;ReBidueB: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 2129-2179, 2181-2235 <HA2>
A,Residues: 2129-2179, 2181-2235 <HA2>
A,Coss-references: GB:MI8471
A,Note: this mRNA from intestine
A,Note: this mRNA from intestine includes a stop codon created by RNA editing in place
R,Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner,
Nucleic Acids Res. 13, 6937-6953, 1985
A,Title: Human apolipoprotein B: identification of cDNA clones and characterization of
A,Reference number: A24269; MUID:86041888; PMID:3903660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stop codon in human intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 3056-3159 eMEH>
A; Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
A; Cross-traferances: GB:X03045; N.; Law, S.W.; Meglin, N.; Brewer Jr., H.
B; Ochem. Biophys. Res. Comun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in
A; Reference number: A29659; MUID:88049670; PMID:2445342
```

```
Pred. No. 6.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P;435-445/Region: receptor binding P;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: apoB
C,Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.6
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| |||||
642 SRLTRKRGLK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 TSĽTRKŘĠĽK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                  A. Reference number: A22006; MUID:84208786; PMID:6373369
A. Accession: A22006
A. Moclecule type: protein
A. Recession: B22006
A. Moclecule type: protein
A. Rolecule type: protein
A. Rolecule type: protein
A. Rolecule type: protein
A. Residues: 3113, 'L', 3115-3130,'R', 3132-3133,'P', 3135-3136,'R' < LEE>
A. Residues: 3113, 'L', 3115-3130,'R', 3132-3133,'P', 3135-3136,'R' < LEE>
A. Title: Structure of the human apolipoprotein B gene.
A. Reference number: A92564; MUID:87057153; PMID:2946672
A. Contents: annoctation; gene structure
R. Magener, R.; Pfitzner, R.; Stoffel, W.
B. A. Title: Studies on the organization of the human apolipoprotein B 100 gene.
A. Reference number: A90715; MUID:87271140; PMID:2886136
A. Title: Studies on the organization of the human apolipoprotein B 100 gene.
A. Reference number: A90715; MUID:87271140; PMID:2886136
A. Title: Alman apolipoprotein B-100 heparin-binding sites.
A. Reference number: A90715; MUID:8728197; PMID:3301850
A. Title: Human apolipoprotein B-100 heparin binding protein.
B. A. Title: Apolipoprotein B-100 heparin binding protein.
A. Reference number: A90125; MUID:6624245; PMID:3081360
A. Contentes annotetation; calcium binding protein.
A. Reference number: A90126; MUID:66242424; PMID:3081360
A. Title: Apolipoprotein B a calcium binding protein.
A. Reference number: A90126; MUID:66242424; PMID:3081360
A. Title: Annotetation; calcium binding protein.
A. Reference number: A90126; MUID:66242424; PMID:3081360
A. Title: Annotetation; calcium binding protein.
A. Reference number: A901869
A. Title: Annotetation; calcium binding protein.
A. Reference number: A901869
A. Title: Annotetation; calcium binding Protein.
A. Reference number: A901869
A. Title: Annotetation; calcium binding Protein.
A. Reference number: A901869
A. Title: Annotetation; calcium binding Protein.
A. Reference number: A901869
A. Title: Annotetation; calcium binding Protein.
A. Reference number: A901869
A. Title: Annotetation; calcium binding Protein.
A. Reference number: B1901869
A. Title: Annotetation; calciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cydaces in Journal of the Society of the Argument of the Argument of the LDI Argument of the LDI Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of the Argument of t
         8
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein B-100 - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 1; Length 4563;
Pred. No. 5.7;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 269,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                    A;Title: Human apolipoprotein B: partial amino acid sequence. A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%; Score 40; DB 2
80.0%; Pred. No. 2.6;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||[ |||||
216 SRLTRKRGLK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
```

RESULT 4

```
apolipoprotein B - golden hamster (fragment)
C; Species: Mesocricetus auratus (golden hamster)
C; Species: Mesocricetus auratus (golden hamster)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C; Accession: JH0102
R; Smith, T.J.
Submitted to GenBank, June 1990
A; Reference number: A38864
A; Recession: JH0102
A; Recession: JH0102
A; Residues: 1-779 cSMI>
A; Residues: 1-779 cSMI>
A; Residues: 1-779 cSMI>
A; Residues: UNIPROT: Q60536; GB: M35187
A; Cross-references: UNIPROT: Q60536; GB: M35187
A; Cross-references: Uniproperties a revision to the sequence from reference JH0101
R; Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A; Title: Sequence of the putative low-density lipoprotein receptor-binding regions of an A; Contents; annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: E60950
R;Law, A.; Scott, J.
A.; J. 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD!
A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: E60950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-275 < LAM>
A;Cross-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A10767
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Croin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable glycosyltransferase STY2310 [imported] - Salmonella enterica subsp. enterica s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2;
Pred. No. 7.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
```

```
A;Status: preliminary
A;Molecule type: DWA
A;Residues: 1-411 < MOL>
A;Cross-references: UNIPROT: P26388
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.5%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.5
ابر 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.5.
To Conservative
              230 RLTEKKGL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||:||
230 RLTEKKGL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLTEKRGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLTEKRGL
                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein wcal [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli 0157:H7, Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D8530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-406 <STO-
A;Coss-references: UNIPROT:Q8X7P5; GB:AE005174; NID:g12516235; PIDN:AAG57104.1; GSPDB:GCGGENETIMENTA
A;Genetimental source: strain O157:H7, substrain EDL933
C;Genetics: Wcal
Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
Reference number: AB0502; MUID:21534947; PMID:11677608
Accession: A10767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:Q8X7P5, GB:BA000007, PIDN:BAB36272.1, PID:g13362317, GSPDB:G
A,Experimental source: strain O157:H7, substrain RIMD 0509952
C,Genetics:
A,Gene: EC92849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cispecies: Escherichia coli (""", """) substrain organia di la coli ("") substrain organia di la coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al coli ("") al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ECs2849 [imported] - Escherichia coli (strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                A,Accession: AI0767
A,Status: prediminary
A,Status: prediminary
A,Molecule type: DAR>
A,Residues: 1-406 «PAR>
A,Residues: 1-406 «PAR>
A,Cross-references: GB:AL513382; PIDN:CAD02463.1; PID:g16503330; GSPDB:GN00176
C,Genetics:
A,Gene: STY2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 406;
                                                                                                                                                                                                                                                                                                                                                  Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2; Length 406;
Pred. No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2;
Pred. No. 25;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%; Score 36;
87.5%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.5
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||:||
230 RLTEKKGL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RLTEKRGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLTEKRGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-406 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLTEKRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
Cispecies: Escherichia coli

Cipate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

Cipate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

Cipate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

Cipate: 12-Sep-1997 #sequence 07-Sep-1997 #text_change 09-Jul-2004

Riblatiner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

A; Reference 277, 1453-1462, 1997

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Reference number: A64720; MUID:97426617; PMID:9278503

A; Reference number: A64720; Muilliary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amsK protein - Erwinia amylovora
C;Species: Erwinia amylovora
C;Species: Erwinia amylovora
C;Species: Erwinia amylovora
C;Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: 561901; 552148
R;Bugert, P.; Geider, K.
Mol. Microbiol. 15, 917-933, 1995
My-Tritle: Molecular analysis of the ams operon required for exopolysaccharide synthesis on A;Reference number: 561891; MUID:9531933; PMID:7596293
A;Accession: 561901
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-407 < 502>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: S15296
R,Jiang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
R,Jiang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
Mol. Microbiol. 5, 695-713, 1991
A;Title: Structure and sequence of the rfb (O antigen) gene cluster of Salmonella seroval A;Reference number: S15296; MUID:91260454; PMID:1710759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: Q46638; EMBL: X77921; NID: 9600426; PIDN: CAAS4889.1; PID: 96004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-406 <BLAT>
A;Cross-references: UNIPROT:P71243; GB:AE000295; GB:U00096; NID:g1788354; PIDN:AAC75105
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Salmonella typhimurium
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 406;
Pred. No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indele
hypothetical protein b2044 - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB 2;
Pred. No. 25;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein - Salmonella typhimurium
```

us-09-823-418-7.rpr

Ŋ

```
15 RLGQKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ठे
                                                                                                                                                                                                                                                                                                                                                                                     arabinan-endo 1,5-alpha-L-arabinase abnA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Baconis E69580
R;Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Garter, N.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Buthors: Founder, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A; Harwood, C.R.; Henaut, A.; Hibbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Labber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell K.; Ribbert, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Socffene, F.; Sekiguchi, J.; Sekweka, A.; Scrot akeuchi, M.; Tamakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Tamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A65580; MUID:98044033; PMID:9384377
A; Reference number: A6580; MUID:98044033; PMID:9384377
A; Redeller, Type: DNA
A; Reference number: Aimerence not shown; translation not shown
A; Reference number: Aimerence not shown; translation not shown
A; Redeller, B.; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors and A; Arthors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:049884; EMBL:U00021; NID:g467141; PIDN:AAA50911.1; rlu:g46714
C;Genetics:
C;Genetics:
A;Start codon: GTG
C;Superfamily: Mycobacterium leprae probable GTP-binding protein; translation elongation
C;Ecywords: duplication; GTP binding; nuclectide binding; P-loop
C;Ecymords: duplication; GTP binding motif b (P-loop)
F;31-38/Region: unclectide-binding motif A (P-loop)
F;140-143/Region: GTP-binding NKXD motif
F;152-154/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P94522; GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14841. A;Beperimental source: strain 168
C;Genetics: A;Gene: abnA
                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable GTP-binding protein - Mycobacterium leprae
NiAlternate names: u0247e protein
C:Species: Mycobacterium leprae
C:Species: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                             ö
Score 36; DB 2; Length 411;
Pred. No. 25;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 2; Length 313;
Pred. No. 31;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Accession: S72953
R, Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A, Description: Mycobacterium leprae cosmid L247.
A, Reference number: S72589
A, Accession: S72953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.48;
70.08;
73.5%;
87.5%;
                                      Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||:|||;
TGLTEERGLR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTEKRGLK 10
                                                                                                                                                                                            235 RLTEKKGL 242
                                                                                                                                                  2 RLTEKRGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <SMI>
   Query Match
                                                                                                                                                      ઠ
                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
probable GTP-binding protein [imported] - Mycobacterium leprae
C;Species Mycobacterium leprae
C;Species Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: F87080
R;Cole, S. T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H.
R; Davies, R.M.; Devlin, K.M.
Nature 409, 1007-1011, 2001
A;Authors Ruter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Statuter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Status: preliminary
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Residue: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <STO>
A;Cross-references: GB:AL450380; NID:913093268; PIDN:CAC31753.1; GSPDB:GN00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ML1372
C;Superfamily: Mycobacterium leprae probable GTP-binding protein; translation elongatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-199 < WOO>
A;Cross-references: UNIPROT:Q9Y7V1; EMBL:AL049498; PIDN:CAB39908.1; GSPDB:GN00068; SPDB
A;Experimental source: strain 972h-; cosmid c645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SPCC645.12c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CiSpecies: Schizosaccharomyces pombe
CiDate: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 09-Jul-2004
CiAccession: T41529
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, March 1999
A;Reference number: 222000
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
F;198-319/Domain: translation elongation factor Tu homology <ET2>F;204-211/Region: nucleotide-binding motif A (P-loop)
F;316-319/Region: GTP-binding NKXD motif
F;349-351/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.4%; Score 34; DB 2; Length 198; 77.8%; Pred. No. 32; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.4%; Score 35; DB 2; Length 462; 77.8%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                         5
                                                                                                                                                      Score 35; DB
Pred. No. 44;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                      Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                            451 RVREKRGLK 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: ||||||
452 RVREKRGLK 460
                                                                                                                                                                                                                                                                           2 RLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: SPDB: SPCC645.12c
```

Search completed: December 29, 2004, 12:39:05 Job time : 10.6591 secs

shigella fl photorhabdu

Q83kj4 Q7n1v8

escherichia salmonella

shigella fl escherichia escherichia

083KJ4
07N1V8
WCAL\_ECCLI
WCAL\_EALTY
07ACP5
07ACP6
08FG31
08Z5H7
08Z5H7
08Z5H7
08Z5H7
08Z5H7
08Z5H7
08Z7H5

salmonella

P71243 P26388 Q7acp5 Q7acp5 Q8E931 Q8E57 Q8E57 Q8E77 Q9E58 Q9E658 Q9E658

escherichia

styela plic arabidopsis

ALIGNMENTS

STYPL

erwinia amy linum usita

```
Name=apoB-100;
Aotus vociferans (Spix's owl monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Aotinee; Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

And the phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AFS48396; AAP97352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein B (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=92075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414
45955 MW; EEFA8492157E1BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
  163
379
404
406
406
406
406
406
406
1112
1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 TRLTRKRGLK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae, Macaca
NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=57176;
Lipoprotein.
NON TER
NON TER 4.
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    028473;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7YQR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                028473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
(028473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 428473
(10 4
                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY SERVICE BY S
  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   013788 homo sapien
072600 homo sapien
072600 homo sapien
07410 diceros bic
079408 hyctimene a
079408 hyctimene a
079407 rousettus a
079708 chaetophrac
071708 chaetophrac
071712 erethizon d
060536 mesocricetu
060537 mesocricetu
07177 gallus gall
071277 gallus gall
071277 gallus gall
079400 tachyglossu
071470 dinomys bra
061622 thermoprote
Bad18908 thermoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bac98534 oryza sat
Q7tn65 atherurus a
Q7tn69 hystrix bra
Q6dcx0 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q61705 thermoprote
Bad18895 thermopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    тасаса faвс
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6zg26 oryza sativ
Bac98516 oryza sat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            ; Search time 58.4091 Seconds (without alignments) 98.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7yqr5 (
Q28473 (
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                 1825181 segs, 575374646 residues
                                                                                                                                               December 29, 2004, 12:13:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q28473
Q13788
APB HUMAN
Q7Z600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q6L6Z2
BAD18908
Q6L705
BAD18895
Q6ZG26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BAC98516
BAC98534
Q7TN65
Q7TN69
Q6DCX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7TN68
Q7YR10
Q7YQM8
Q7YQM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7YR04
Q7YR08
Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q60536
Q60537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07YQN2
07YQM9
07YQN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7TN72
                                                                                                                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07YQR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27LZ77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                  US-09-823-418-7
49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                          1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UniProt_02:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400
                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein
                                                                                                                                                                                                                                                                              Seguence:
                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                                                   ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ģ
```

ö

Gaps

ö

Score 44; DB 2; Length 414; Pred. No. 2.5; 0; Mismatches 1; Indels

PRT;

```
Zannis V.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APB_HUMAN STANDARD; PRT; 4563 AA. P06114; O00502; Q13787; 01.NOV-1986 (Rel. 03, Created) 01-NOV-1986 (Rel. 03, Last sequence update) 05-NUL-2004 (Rel. 44, Last sequence update) 05-ULD-2004 (Rel. 44, Last annocation update) 05-ULD-2004 (Rel. 44, Last annocation update) 05-ULD-2004 (Rel. 44, Last annocation update) 05-ULD-2004 (Rel. 44) Last annocation update) 05-ULD-2004 (Rel. 44) Last annocation update) 05-ULD-2004 (Rel. 44) Last annocation 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains: Apolipoprotein 05-ULD (Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=87191999; PubMed=2883086;
Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                           ö
metabolism in the cynomolgus monkey: evidence for post-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 2; Length 3262;
Pred. No. 20;
                                                                                                                                                                                                                                                         Length 596;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                  Murray R.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3262 AA; 370140 MW; 56603BC0618DD40D CRC64;
                                                                                                                                                                                 1 1
596 596
596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
GO; GO:0006869; P:lipid transport; NAS.
NON_TER
                                                                                                                                                                                                                                                      89.8%; Score 44; DB 2; 90.0%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 3262 AA.
                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                   transcriptional regulation.",
Biochim. Biophys. Acta 1086:326-334(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the B-74 region.";
Gene 49:29-31 (1986).
EMBL; M15421; AAA51758.1; -.
PIR; A27850; LPHUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24, APOB protein (Fragment).
                                                                                                                                     EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                                                                                                    Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2084 TRLTRKRGLK 2093
                                                                                                                                                                                                                                                                                                                                                      226 TRLTRKRGLK 235
                                                                                                                                                                                                                                                                                                                        1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                      TISSUE=Liver;
                                                                                                                                                                     Lipoprotein.
NON TER
                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=APOB;
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q13788
Q13788;
 "Apo B
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APB_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSSUBBLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
"The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEDLINE=85300528; PubMed=2994225;
MEDLINE=85300528; PubMed=2994225;
Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priestley L.M., Robertson B., Rall L.B., Betsholtz C., Shows T.B.,
Mahley R.W., Scott J.;
"Human apolipoprotein B: structure of carboxyl-terminal domains, sites
of gene expression, and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE=87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
Gotto A.M. Jr., chan L.;
Gotto A.M. Jr., chan L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE OF 3056-3159 FROM N.A.
MEDLINE=86041889; PubMed=3903660;
Mehrablan M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNA.";
                                                                                                                                                    MEDLINE-87016385; PubMed-3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
MEDLINE-86093680, PubMed=3841204;
CarlBeon P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
Bjursell G.,
"Molecular cloning of human apolipoprotein B cDNA.";
Nucleic Acids Res. 13:8813-8826(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J., Lee N., Brewer H.B. Jr., "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino acid sequence.", Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE-88003974; PubMed-3652907;
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
DNA 6:363-372 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M., Nolte R.T., Atkinson D.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 709-906 FROM N.A.
MEDLINE=85270450; PubMed=3860836;
Deeb S.S. Motulaky A.G., Albers J.J.;
"A partial cDNA clone for human apolipoprotein B
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 13:6937-6953(1985).
                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 14:7501-7503(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 261:12918-12921(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87161758; PubMed=3030729;
Cladaras C., Hadzopoulou-Cladaras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=87041416; PubMed=3464946;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                    NCBI_TaxID=9606;
```

```
VARIANT LEU-2739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=APOB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7Z600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  072600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07Z600
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                       Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V., Chen G.C., Kirsher S.W., McEnroe G., Kane J.P., "Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lie F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.; "Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100.";
Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                        MEDLINE=88618019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.,
"Apolipoprotein B-48 is the product of a messenger RNA with an organ-
specific in-frame stop codon.";
science 238:363-366(1987).
                                                                                                                                                                                                                                                                                                                                            MEDLINE=87039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
Levy-Wilson B., Scott J.;
"Complete protein sequence and identification of structural domains of human apolipoprotein B.";
Nature 323:734-738(1986).
                                                                                                   SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE=86287319; PubMed=3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M. Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of CDNA clones encoding the entire B-26 region of human apolipoprotein B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91071750; PubMed=1979313;
Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.;
"Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene.";
Hum. Genet. 86:91-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89098975; PubMed=2563166;
Soria L.F., Ludwig B.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20143590; PubMed=10679026; Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.; Fallicojation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and triglycerides.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprotein B is a calcium binding protein.";
Biochem. Biophys. Res. Commun. 137.499499(1986).
                                                               apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682 (1986)
                                                                                                                                                                                                              SEQUENCE, AND IDENTIFICATION OF APO-B48.
             GEDLINE=86149325; PubMed=3513177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Cell 11:721-734(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITOYLATION OF CYS-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALCIUM-BINDING DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT FDB GLN-3527.
                                                                                                                                                                                                              PARTIAL SEQUENCE,
MEDLINE=88018019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT SER-4338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAINS
```

```
hypocholesterolemia.";
Hum. Genet. 102:44-49(1998).
-!-FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apol B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G., Krempf M., Girandet P., Junien C., Boilau C.; "Familial ligand-defective apolipoprotein B-100: simultaneous detection of the ARG3500--AGLN and ARG3531---CYS mutations in a French
                                                                                                                                                                                                      MEDLINE=95190020; PubMed=7883971;
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
"Familial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
J. Clin. Invest. 95:1225-1234(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
AND THR-4481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432 AND ILE-3921.
MEDLINE-9811125; PubMed=9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97044521; PubMed=8889592;
Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
MEDLINE=91016974; PubMed=2216805; Huang L.-S., Gavish D., Breslow J.L.; Haang L.-S., Gavish D., Breslow J.L.; Sequence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A.,
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Apolipoprotein B (Including Ag(X) antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS FDB GLN-3527 AND CYS-3558.
MEDLINE=97403938; PubMed=9259199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR-SSCP.";
Hum. Mutat. 8:282-285(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 25, C
(TrEMBLrel. 25, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003
01-OCT-2003
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    population.
```

ö

ö

Gape

ö

ઠે g

us-09-823-418-7.rup

```
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Wadsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
"I newloce for Eutherian relationships.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nyctimene albiventer (Common tube-nosed fruit bat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Nyctimene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
Am New phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pteropūs hypomelanus (Small flying fox).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;
                                                                                                                                    81.6%; Score 40; DB 2; Length 432;
80.0%; Pred. No. 18;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.6%; Score 40; DB 2; Length 436; 80.0%; Pred, No. 18; 1; Mismatches 1; Indels
                                                                                                   432 AA; 48171 MW; F27B7AB39604732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 1
436 436
436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                 436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 AA
         Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AY243375; AAP50763.1; -.
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                  Query Match
Best Local Similarity 80.0
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 80.0 es 8; Conservative
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                             275 SRLÍRKRGÍK 284
                                                                                 432
                                                                                                                                                                                                              1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||| |||||
279 SRLTRKRGLK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pteropodinae; Pteropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9405;
                                          Lipoprotein.
NON TER
NON TER
SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein.
NON TER
NON TER
SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                           Q7YQM8
Q7YQM8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07YQM7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7YQM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
Q7YQM7
                                                                                                                                                                                                                                                                                                                         STTTS
                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
Apolipoprotein B (Fragment).
Agolipoprotein B (Fragment).
Balaucomys volans (Southern flying squirrel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Sciuridae, Petauristinae,
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22761261; PubMed=12878460; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; "A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Diceros bicornis (Black rhinoceros).
Bukaryotes, Netazzos, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Diceros.
                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                          Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 2; Length 421; Pred. No. 17; 1 Mismatches 1; Indels
                                                                                                                                                                 4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 421
421 AA; 46747 MW; D47B77BD4F864FD1 CRC64;
               GO; GO:0005319; F:lipid transporter activity; IEA. GO; GO:006669; P:lipid transport; IEA. InterPro; IPR009454; DUP1081.
InterPro; IPR00147; Lipid_transprt_N. Pfam; PF06448; DUF1081; 1.
Pfam; PF01449; Vitellogenin_N; 1.
                                                                                                                                                                                                    89.8%; Score 44; DB 2;
90.0%; Pred. No. 28;
iive 0; Mismatches I
                                                                                                                                                                                                                                                                                                                                                                                                               421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
EMBL; AY324608; AAP72970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.6%;
80.0%;
                                                                                                                        SMART; SMOO638; LPD N; 1.
                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                               3385 rkirkkicik 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||| |||||
264 SRLTRKRGLK 273
                                                                                                                                                                                                                                                                              1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTEKRGLK 10
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=64683;
                                                                                                                                                  Lipoprotein.
SEQUENCE 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      poprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glaucomys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              Q7TN68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7YR10,
                                                                                                                                                                                                                                                                                                                                                                                                           Q7TN68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7YR10
                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
Q7YR10
```

à

ö

ô

S

ö

Gaps

ö

Indels

SO FT SO

Q7YR04

ò 셤

```
MEDLINE-22761261; PubMed=12878460;
MEDLINE-22761261; PubMed=12878460;
Manrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker; apolipoprotein B, provides compelling evidence for eutherian relationships.",
Mol. Phylogenet. Bvol. 28:225-240(2003).
EMBL; AY23369; AAPSO757.1, ...
InterPro: IRR00871; Beta lactamase A.
PROSITE; PS00146; BETA LACTAMASE A; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-2761261, PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apolipoprotein B (Fragment).
Hydrochoerus hydrochaeris (Capybara) (Carpincho).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Agouti paca (Paca).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Agoutidae, Agouti.
NCBI_TaxID=108852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.6%; Score 40; DB 2; Length 445; 80.0%; Pred. No. 18; tive 1; Mismatches 1; Indels
                                                     81.6%; Score 40; DB 2; Length 445; 80.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 1
445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
  445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TEMBLrel. 26, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apolipoprotein B 100 (Fragment).
                         Query Match
Best Local Similarity 80.00,
Best Local Similarity 80.00,
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                              :||| |||||
288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 SRLTRKRGLK 297
                                                                                                                                                                1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein.
NON TER
NON TER
SEQUENCE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrochaerie
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                     Q7TN64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07TN71;
                                                                                                                                                                                                                                                                                                                                                   Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7TN71
                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                         DDT ACCOUNT BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolitoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AX243383; AAP50771.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-2761261. PubMed=12878460,

Amrine-Madeen H., Koopfili K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolipoprotein B, provides compelling

worldene for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243378; AAPS0766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rousettus amplexicaudatus (Common rousette).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Rousettus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apolipoprotein B (Fragment).
Abelophractus villosus (South American armadillo).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                          Score 40; DB 2; Length 438;
Pred. No. 18;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%; Score 40; DB 2; Length 438;
80.0%; Pred. No. 18;
rative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1
438 438
438 AA, 48597 MW, 41C890DEAF95C872 CRC64;
                                                                                                          438 AA; 48734 MW; 2BD85BCBF4E2CC41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                81.6%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
     EMBL; AF548436; AAP97392.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apolipoprotein B (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.v.
Best Local 8; Conservative
                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                         :||| ||||
281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 SRLTRKRGLK 290
                                                        1
438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1445
                                                                                                                                                                                                                                                                          1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=29080;
                                                     1
438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipoprotein.
NON TER
NON TER 44
                            Lipoprotein.
NON TER
NON TER 4
SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7YR08
Q7YR08;
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
```

27YR08

ઠે

ö

Gaps

ö

```
g
                                                   ò
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=90236327; PubMed=2332175;

Smith T.J., Hautamaa D., Maeda N.;

Sequence of the putative low-density lipoprotein receptor-binding regions of apolipoprotein B in mouse and hamster.";

Gene 87:309-310 (1990).

EMBL; M35187; AAA37059.1; -.

PIR; C60950; C60950.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An wy phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                      Erethizon dorsatum (North American porcupine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Hystricognathi, Erethizontidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
            81.6%; Score 40; DB 2; Length 445; ilarity 80.0%; Pred. No. 18; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

81.6%; Score 40; DB 2; Length 445;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                     1 1
445 445
445 AA; 49617 MW; 9572FESF5E7625F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 1
780 780
780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                          445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                780 AA
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                     :||| |||||
288 SRLTRKRGLK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||| |||||
288 SRLTRKRGLK 297
                                                        1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TRLTEKRGLK 10
Query Match
Best Local Similarity
18, Conserve
                                                                                                                                                                                                                                                     NCBI_TaxID=34844;
                                                                                                                                                                                                                                                                                                                                                           Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein.
NON TER
NON TER 7
SEQUENCE 78
                                                                                                                                                                                                                                                                                                                                                                     NON TER
NON TER
SEQUENCE
                                                                                                                                     Q7TN72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260536
                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                            셤
                                                                                                                                                 ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ద
```

```
Query Match 81.6%; Score 40; DB 2; Length 780;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps
```

ö

1 TRLTEKRGLK 10 :||| ||||| 642 SRLTRKRGLK 651 Search completed: December 29, 2004, 12:37:34 Job time : 59.5202 secs

```
December 29, 2004, 12:10:41; Search time 61.027 Seconds (without alignments) 58.786 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                2002273 segs, 358729299 residues
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                              US-09-823-418-8
50
                                                                                                                                                                                                                                                       1 TRLTDKRGLK 10
                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                           Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\*

geneseqp20048:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Database

#### Aay30689 Apo-B100 Aay30688 Apo-B100 Aaw57207 Apo B bin Aaw57207 Apo B 100 Aaw41261 Apolipopr Aaw56892 ApoB-100 Aaw57208 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw64867 Nucleic a Aaw66876 Nucleic a Aby37687 Peptide # Abg52504 Human apo Aav96876 Nucleic a Abg52504 Human apo Aar374031 Sequence Adj57400 Human apo Aar31237 Human Apo Aay31237 Human Apo Aay31237 Human Apo Aay31237 Human Apo Aay31262 Apolipopr Aaw96826 Amino aci Aaw96826 Amino aci Aaw96826 Amino aci Aaw96826 Amino aci Aaw96826 Amino aci Apo-B100 Apo B bin Apo B 100 Human apo Nucleic a Peptide # Apo B 100 Apo B 100 Human apo Sequence Human apo Human Apo Description SUMMARIES AAE14541 AAW96876 AAW64587 AAW96845 AAR72704 AAR34031 ADJ57400 AAW57208 AAW57209 AAU98981 ADD48677 AA015893 ABR40253 AAW96892 ABJ37575 **ABB37687** ABG52504 В Query Match Length 2463 3923 4536 4536 4561 4563 4563 343 Score Result 8

Abu79140 Apolipopr Adf43408 Apolipopr Adh18871 Human apo Adh18870 Human apo	Human Human Novel	4 .4 .4 .	Aagsysiq Arabidops Aags7s61 Arabidops Aags9301 Arabidops Aay30682 AppR100		
ABU79140 ADF43408 ADH18871 ADH18870	AD033445 AD033447 AAU33184	AAGS9302 AAGS9302	AAG39914 AAG57561 AAG59301 AAY30682	AAY30687 AAY30690 AAY30692	AAY30686 AAW57206 AAW87717
4563 6 4563 7 4563 8 4563 8	4563 8 4563 8 4590 4	132 3	150 3 150 3	2222	1110
8 8 8 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		78.0	78.0	7.4.0 0.4.0	74.0 74.0 74.0
4 4 4 4	2 4 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	. e e e		333	37 37
22 2 2 4 2 4 2 4 4 4 4 4 4 4 4 4 4 4 4	32	1 2 2 4 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1 5	3 3 3 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 0 1 0	4 4 4 5 4 5

#### ALIGNMENTS

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation, atherosclerosis, low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Ź AAY30689 standard; peptide; 10 99WO-US004805 98US-0077618P Boren JOS; (REGC ) UNIV CALIFORNIA WPI; 1999-551509/46. Innerarity TL, Ното варіенв WO9946598-A1 05-MAR-1999; 10-MAR-1998; 16-SEP-1999 Synthetic AAY30689; RESULT 1 AAY30689 

Claim 17; Page 57; 70pp; English.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of aposl100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

~

us-09-823-418-8.rag

Sequence 10 AA;

ö

Gaps

.;

```
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                            Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                    Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                     100.0%; Score 50; DB 2; Length 10; 100.0%; Pred. No. 0.0029; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                               AAY30688 standard, peptide, 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0077618P
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Innerarity TL, Boren JOS;
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                   TRLIDKRGLK 10
                                                                                                                                                                         1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-551509/46.
                                                                                                     Query Match
Best Local Similarity
                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                              17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-1998;
                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                        AAY30688;
                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                        AAY30688
                                                                                                                                                                                                                                            8888888888
                                                                                                                                                                        셤
                                                                                                                                                  ò
```

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which compounds the method comprises detecting compounds which affect to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the also be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the formation of atheroselerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal Claim 17; Page 57; 70pp; English.

1 TRLIDKRGLK 10

H

2 TRLTRKRGLK

요 ઠ

```
The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) that express an apo B protein receptor, and (ii) additives for calls culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                       Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide binding to apo B protein delivering drugs to cancer cells
                                        барв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
        Length 10;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 42; DB 2; Length 11; 90.0%; Pred. No. 0.14; ive 0; Mismatches 1; Indels
                                      .,
      Score 46; DB 2;
Pred. No. 0.019;
                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.
                                                                                                                                                                           AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 52; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baillie
                                                                                                                                                                                                                                                                         Apo B binding site peptide 2.
      92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96GB-00020153.
                                                                                                                                                                                                                                         03-AUG-1998 (first entry)
Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                  1 TRLIDKRGLK 10
                                                                                 ||||:||||
1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                           AAW57205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches
                                                                                                                                             RESULT 3
                                                                                                                                                                                                          ð
                                                                                               셤
```

AAW57207;

```
This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, consecutable to a tribe retaining anti-coagulant properties of appolipoprotein B-100 (appel-100). Z1-KAQ-X1-KKNKHRHS-X2-T-Z2 (I) X1 = S or compositions containing the peptide, or 1-47 amino acids (as); Z2 = the C terminus of the peptide, or 1-47 amino acids compositions containing the peptide are used for simultaneous, caparate or sequential treatment of cancer, particularly to prevent compositions containing the peptide are used for simultaneous, caparate or sequential treatment of cancer, particularly to prevent compositions contained to reduce the protein or sequential treatment of cancer, particularly to prevent composition or after surgery or in cases of heart attack, stroke etc.) and to inhibit anglogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits continuate complex; and prevents activation of the protromominase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much composited than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                               Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 22, 60pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW96892 standard, peptide; 15 AA.
                                                                   Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        97WO-GB001255
                                                                                                                                                                                                                                                                                                                                                                                                                                                        96GB-00009702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ettelaie C;
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                        prothrombinase complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15 AA;
                        19-MAY-1998
                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                          W09743311-A1
                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                         20-NOV-1997.
                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW96892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96892
ID AAW9
XX
AC AAW9
XX
XX
XX
XX
XX
XX
XX
XX
XX
XX
XX APOB
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KAEYKKKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-teargeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                                                      Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 13;
Pred. No. 0.16;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "attached to retinoic acid"
                                                                                                                                                                                                           Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baillie G;
                                                                   AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that express this receptor.
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TRLTRKRGLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1996;
                                                                                                                                                               03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halbert GW,
                                                                                                                                                                                                                                                                                                                                                         Synthetic.
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                   Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;
                                       Gaps
                                                                                                                                                                                                                                                                                                                                             ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                       ;
0
  Length 15;
                                     1; Indels
Score 42; DB 2;
Pred. No. 0.19;
0; Mismatches
```

AAW41261;

RESULT 5 AAW41261

셤 ઠે

Matches

4

us-09-823-418-8.rag

```
The invention relates to a novel ligand for binding a target blomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                           Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 42; DB 6;
llarity 90.0%; Pred. No. 0.26;
Conservative 0; Mismatches
                                                                                                         Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57208 standard, peptide, 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                    Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baillie
           20-JUL-2001; 2001US-0306726P.
                                                                                                      Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Owens MD,
                                                                                                                                          WPI; 2003-300420/29.
                                                ETH ZUERICH
UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57208;
                                                (ETHZ-) 1
(UYZU-) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
             ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein number of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The appolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of fibrosis and arteriosclerosis
apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytobtatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 42; DB 2; Length 15; 90.0%; Pred. No. 0.19; 1; Indels .ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                      Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                           97US-00874807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUL-2002; 2002WO-US023419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003007689-A2
                                                                                                                                                                                                                         13-JUN-1997;
14-MAY-1998;
                                                                                                               WO9856938-A1
                                                                                                                                                                                      10-JUN-1998;
                                                                             Homo sapiens
                                                                                                                                                17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                    Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2003
```

ABJ37575;

RESULT 7

셤

ö

Gaps ö

Length 20; 1; Indels

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein ceeptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKKHRH (1) or THLTRKRGLK (2), or their consection as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cancer cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles are for call culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                      DB 2; Length 22;
                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                       0.28;
                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.28
0; Mismatches
                                                                                                                                                                                                                                                                                                                                    84.0%; Score 42; 90.0%; Pred. No. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW57209 standard; peptide; 22 AA.
              Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                           TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                      Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57209;
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
```

ð

The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)

Claim 13; Fig 7; 73pp; English.

that express this receptor.

Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells

ö

Baillie

Owens MD,

Halbert GW,

WPI; 1998-230637/20.

```
ö
particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDb), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDb. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDb. in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                   84.0%; Score 42; DB 2; Length 22; 90.0%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                            1,
                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE14541 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Narvanen O, Yla-Herttuala S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            7 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-179777/23.
                                                                                                                                                                                                                                                                               Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200206314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lipoproteín.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE14541;
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE14541
        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
```

φ

```
Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.
                                                                                                                                                                                       Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
                                                                                                                                                              Human apolipoprotein peptide fragment #1.
                                                                            AAW64587 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 9; 18pp; German.
        11 TRLTRKRGLK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                Moritz B, Kiessig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-416142/36.
                                                                                                                                                                                                                                                                                                                                                                                                     (IMMO ) IMMUNO AG.
                                                                                                                                  23-OCT-1998
                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                               12-JAN-1998;
                                                                                                                                                                                                                                                                                        EP857973-A2
                                                                                                                                                                                                                                                                                                                    12-AUG-1998
                                                                                                         AAW64587;
                                                  RESULT 12
                                                               AAW64587
                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very low density lipoproteins (VLDL), intermediate density lipoprotein (VLDL), low density lipoproteins (LLDL) and lipoprotein a The present sequence can be used in the composition of the invention. The present apportation describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in viro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                      Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                      Gaps
                                                                                                      ö
                                                                                                                                                                                                                                                                                                          Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                         Length 34;
                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%; Score 42; DB 2; Length 36; 90.0%; Pred. No. 0.47;
                                                                         DB 5;
                                                                                     0.45;
                                                                      Score 42; DB E
Pred. No. 0.45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moore JP;
                                                                                                                                                                                                                           AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16, Fig 12C, 293pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                        84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00874807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoogeveen RC,
                                                                                                                                                                                                                                                                                22-APR-1999 (first entry)
                                                                                                  9; Conservative
                                                                                                                             1 TRLIDKRGLK 10
                                                                                                                                                        34
                                                                                                                                                       25 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-070331/06.
                                                                   Query Match
Best Local Similarity
                                          Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment.
                                                                                                                                                                                                                                                     AAW96876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                               Matches
                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                AAW96876
                                                                                                                             ò
                                                                                                                                                       ద
```

>

Lang H,

98EP-00890007.

(first entry)

```
ö
                                                                                                                                                                                                                                                                                                                                                                           (associated with hypercysteinaemia and venous thrombosis) and factor VII mutations (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method does not require complex apparatus for polymerase chain reactions, it is simple, standardisable and reliable and is particularly suited to routine screening. It also allows mutant protein
AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are appecially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain alleles of apol indicates increased risk of deep alleles of abol indicates increased risk of developing Alzheimer's disease), thermostable 5,10-methylenetetrahydrofolate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 2; Length 37;
Pred. No. 0.49;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96845
ID AAW96845 standard; peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in a sample to be quantified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

ö

Gaps

ö

1; Indels

0; Mismatches

Best Local Similarity 90.0 Matches 9, Conservative

1 TRLTDKRGLK 10

ઠે

```
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 31152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG52504 standard; peptide; 343 AA.
                                                                                                                                                                                 26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0201456P.
30-UIN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00533366.
21-SEP-2000; 2000US-023468IP.
27-SEP-2000; 2000US-023468IP.
04-OCT-2000; 2000GS-0032459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                       30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 İRLİRKRĞLK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 343 AA;
WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG52504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
ABG52504
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       applipation of application of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t
                                                                                                                                                                              Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW96827-77 represent nucleic acid binding domains derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #5193 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 42; DB 2 90.0%; Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                 Nucleic acid binding domain from apoB-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 151; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB37687 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-00874807.
98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoogeveen RC,
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-070331/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 51 AA;
                                                                                                                                                                                                                                                                                                                              Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                 WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-1997;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                             22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment.
                      AAW96845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB37687
```

Best Loc Matches

8

ö

Gaps

.. 0

Penn SG,

(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR; Hanzel DK,

WPI; 2001-488898/53

n genome-derived single exon nucleic acid probes useful for analyzing expression in human adult liver. gene

Claim 27; SEQ ID NO 31152; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult

1 iver. comprising one of 11109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high erringency to a nucleic acid molecule expressed in the human adult liver.

2. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published\_pot\_sequences 

Sequence 343 AA;

Gaps · 0 84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 5.1; tive 0; Mismatches 1; Indels Query Match Best Local Similarity 90.0° Matches 9; Conservative

ö

1 TRLIDKRGLK 10 ò

169 TRLTRKRGLK 178 셤

Search completed: December 29, 2004, 12:28:50 Job time : 62.0227 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 29, 2004, 12:15:57 ; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-8 50 1 TRLTDKRGLK 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scrip	apolipoprotein B -	apolipoprotein B-1	Д	apolipoprotein B -	apolipoprotein B-1	probable periplasm	imidazoleglycerol-	sugar binding prot	multiple sugar-bin			phosphotransferase	probable phosphotr	ganciclovir kinase	glutamine-fructose	btuR protein (impo	hypothetical prote	-	sodium/pantothenat	probable anthranil	hypothetical prote	hypothetical prote	•-	probable helicase	189.6K hypothetica	hypothetical prote	probable succinate		probable glycosylt
SUMMARIES	Ð	532802	LPHUB	C60950	JH0102	E60950	A43654	D90206	AC2865	B97642	S17648	S17649	QQBEHS	T44214	T44029	B81246	T44695	T01873	H82022	F97787	T00782	F86359	T01955	H84486	F84517	D86481	T48965	G81138	S58205	AI0767
	Length DB	!			σ.			193 2						563 2					612 2			1029 2	073	241	1265 2	678	752		360 2	
de	ដូម	84.0	84.0	76.0	76.0	72.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0		66.0	0.99	0.99
	Score	42	42	38	38	36	35	35	35	35									34	34	34	34	34	34	34	34		33	33	33
	Result No.	1	71	m	4	D.	9	7	<b>6</b> 0	σ	10	11	12	13	14		16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	hypothetical prote	hypothetical prote	amsK protein - Erw	hypothetical prote	hypothetical prote	fimbrial assembly	apolipoprotein B -	RNA polymerase bet	RNA polymerase bet	DNA-directed RNA p	DNA-directed RNA p	DNA-directed RNA p	probable large Pro	hypothetical_prote	DNA topoisomerase
A90985	D85830	C64970	S52148	S15296	T21384	F82546	865460	A86501	D72122	G81686	H71529	F81548	T35985	G87376	PN0152
N	~	N	N	N	~	N	N	N	N	7	N	N	~	C3	7
406	406	406	407	411	487	490	1058	1252	1252	1252	1252	1262	1366	84	122
0.99	0.99	0.	0.	0.	٥.	0.99	٥.	٥.	٥.	٥.	٥.	٥.	٥.	۰.	٥.
99	99	99	99	99	99	99	99	99	99	99	99	99	99	64	64
33	33	33	33	33	33	33	33	33	33	33	33	33	33	32	32

### ALIGNMENTS

```
apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 832802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchir Blochim: Blophys- Acta 1086, 325-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: 832802; MUID:92075708; PMID:1742325
A;Accession: 832802
A;Accession: 832802
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residuae: 1-59 cAPA
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301
C;Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 596;
Pred. No. 1.8;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0
Matches 9; Conservative
```

apolipoprotein B-100 precursor - human N;Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74 C;Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004 C;Accession: A27850; A25679; Ā25263; A25266; A24320; A24684; A23817; A25774; A2 C;Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A2 R;Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sc DNA 6, 363-372, 1987

A;Title: DNA sequence of the human apolipoprotein B gene.
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Accession: A27850
A;Accession: A27850
A;Accession: A27860
A;Accession: A27, A7, 619-1929, F7, 1931-3318, D7, 3320-3426, T7, 3428-3431, O,, 3433-3731, A;Residues: 1-617, A7, 619-1929, F7, 1931-3318, D7, 784819; UNIPROT:09UMNO; UNIT. B;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: r
A;Reference number: A91058; MUID:87161758; PMID:3030729

A;Molecule type: mRNA A;Residues: 1-11,15-2539, 'S',2541-3823,'R',3825-4563 <CLA> A;Note: 1109-Asp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

Dec

J.T.

```
R;Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E. Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than o. A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Residues: 3846-4298 «SHO>
A;Residues: 3846-4298 «SHO>
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
B;Pfitzner, R.; Wagener, R.; Stoffel, W.
A;Reference number: A25572; MUID:87076044; PMID:3024665
A;Accession: A25572
A;Accession: A25572
A;Accession: A25572
A;Accession: A25572
A;Accession: A25572
A;Accession: A25572
A;Accession: A25572
A;Accession: A25573
A;Residues: 4219-4337, S', 4339-4563 «PFI>
A;Cross-references: GB:W36676
R;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
A;Reference number: A24738; MUID:86042646; PMID:2932736
A;Recenter number: A24738; MUID:86042646; PMID:2932736
A;Accession: A24738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: mRNA
A Reaidues: Nv. 3733-331, I', 3733-3875, Av., 3847-3948, 'F', 3950-3963, 'Y', 3965-3982,'S', 39
A; Keaidues: Nv. 3729-3731, I', 3733-3805, Br. 3745. 1; PID: G178736
A; Croen. S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cai'
Science 238, 363-366, 1987
A; Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
A; Reference number: A40133; MUID: 88018019; PMID: 3659919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B4033
A; Residues: 2165-2179 < CH1>
A; Residues: 2165-2179 < CH1>
A; Residues: 2165-2179 < CH1>
A; Residues: 2165-2179 < CH1>
A; Residues: 2165-2179 < CH1>
A; Rocession: A40133
A; Rocession: A40133
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55
36;1486-1498;1537-1556;1563-1572;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-
A; Note: these fragments were derived from apo48
R; Note: these fragments were derived from apo48
R; Note: these fragments were derived from apo48
R; Note: these fragments were derived from apo48
R; Reference number: A.28 1911-110; 1987
A; Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism F
A; Reference number: A28002
A; Molecule type: mRNA
A; References: 2129-2179, 2181-2235 cHA2>
A; Residues: 2129-2179, 2181-2235 cHA2>
A; Residues: 2129-2179, 2181-2235 cHA2>
A; Residues: 2129-2179, 2181-2235 cHA2>
A; Residues: 213-2181-2335 cHA2>
A; Residues: 213-2181-2335 cHA2>
A; Residues: 213-2181-235 cHA2>
A; Residues: 213-2181-235 cHA2>
A; Residues: 213-2181-235 cHA2>
A; Residues: 213-2181-235 cHA2>
A; Residues: 213-2181-235 cHA2>
A; Residues: 213-219, 2181-235 cHA2>
A; Righerantal source: intestine includes a stop codon created by RNA editing in place C R; Merkerence number: A24269; MUID:86041889; PMID:3903660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA AROSA AROSA ARREAGUES 1196-2179 A.00SA ARREAGUES 2.165-2.219 A.00SA ARREAGUES 2.165-2.219 A.0SA ARREAGUES 2.165-2.219 A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.0SA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OSA A.OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human apolipoprotein B 100-ape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 3056-3159 <MEH>
A;Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
A;Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
R;Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem. Biophys. Res. Commun. 148, 279-285, 1997
A;Title: Identification of a novel in-frame translational stop codon in human intestine
A;Reference number: A29659; MUID:88049670; PMID:2445342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B40133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A24269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A29659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: A35783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A22266
A.Accession: A22266
A.Accession: A22266
A.Accession: A22266
A.Accession: A22266
A.Accession: A2226
A.Accession: A2226
A.Accession: A2226
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accession: A2230
A.Accessio
                                                                                                                                                                                              A; Rolecule type: mRNA
A; Residues: 1-272, N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679,'Q'
A; Residues: 1-272, N', 274-617, 'A', 619-1217, 'E', 1219-2091, 'V', 2093-2364, 'T', 2366-2679,'Q'
A; Croseraces: GBIX04566; NID: 834331
R; Law, S.W.; Grant, S.M.; Higuchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Title: Human liver apolitoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID: 87041416; PMID: 3464946
A; Accession: A2267
A; Molecule type: mRNA
A; Residues: 1-617, 'A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866,'G', 1868-2036,'N', 24189-4220,'M', 4222-4563 cLAW>
A; Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chem. S.H.; Yang, C.T.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
J. Biol. Chem. 261, 12918-12921, 1986
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID: 87008488; PMID: 3759943
A; Accession: A2526
A; Molecule type: mRNA
A; Residues: 1-97, 'I', 99-328,'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-
                                                  human apolipoprotein B-100.
A)Reference number: A93639; MUID:87016385; PMID:3763409 A)A)Accession: A25263
```

```
Cypecies: Mesocriccus auratus (golden hamster)
Cypecies: Mesocriccus auratus (golden hamster)
Cypecies: Mesocriccus auratus (golden hamster)
Cypecies: J7-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
Cypecies: J70102
Rysmith, T.J.
Ayreference number: A38864
Ayreference number: A38864
Ayreference number: A38864
Ayreference: J702 cSMI>
Ayreferences: UNIPROT:Q60536; GB:M35187
Ayreferences: UNIPROT:Q60536; GB:M35187
Ayreferences: UNIPROT:Q60536; GB:M35187
Ayreference: Linis is a revision to the sequence from reference J40101
Rysmith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
Ayritle: Sequence of the putative low-density lipoprotein receptor-binding regions of any Ryseference number: J40101; MUID:90236317; PMID:2332175
Ayreference number: J40101; MUID:90236327; PMID:2332175
Ayreference number: J40101; MUID:90236327; PMID:2332175
Ayreference number: J40101; MUID:90236327; PMID:2332175
Ayreference number: J40101; MUID:90236327; PMID:2332175
Ayreference number: J40101; MUID:90236327; PMID:2332175
Ayreference number: J40101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein F;435-445/Region: receptor binding F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B60950
R;Law, A.; Scott, J.
Lipida Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD<sup>1</sup> A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: B60950
A;Accession: B60950
A;Accession: B60950
A;Accession: B60950
A;Cross-references: UNIPROT:07LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable periplasmic receptor protein chvE precursor - Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 09-Jul-2004 C; Accession: A43654 #sequence_revision 20-Feb-1993 #text_change 09-Jul-2004 C; Accession: A43654; MulD: 1990 W:; Nester, E.W.
J. Bacteriol. 172, 1814-1822, 1990
A; Fitule: A chromosomal Agrobacterium tumefaciens gene required for effective plant sign A; Accession: A43654
A; Accession: A43654
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB
Pred. No. 15;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                  (fragment)
                                                              apolipoprotein B - golden hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: apoB
C,Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 TSLTRKRGLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             642 SŘĽTRKŘĠĽK 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
A; Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su FileBost Lett. 170, 105-108, 1964

RieleBost Lett. 170, 105-108, 1964

A; Title: Human apolipoprotein B partial amino acid sequence.

A; Reference number: A22006; MUID: 84208786; PMID: 637389

A; Accession: A22006

A; Accession: A22006

A; Accession: Detain

A; Residues: 873-892, K; 694-896 «LEI>
A; Residues: 873-892, K; 694-896 «LEI>
A; Residues: 873-892, K; 694-896 «LEI>
A; Residues: 873-892, K; 694-896 «LEI>
A; Residues: 873-892, K; 694-896 «LEI>
A; Residues: 3113, Li Ludvig; E. M.; Pierotti, V.R.; Calati, L.; Omasch, M.A.; Wallis, S.C.; J. Blool. Chem. 261, 13364-13367, 1396

A; Residues: 3113, Li Jails-3130, K; 7312-3133, P; 7313-3136, K; 4.EE>

R; Residues: 3113, Li Jails-3130, R; Pierotti, V.R.; Calati, L.; Omasch, M.A.; Wallis, S.C.; J. Biol. Chem. 261, 13364-13567, 1396

A; Title: Structure of the human apolipoprotein B 100 gene.

A; Reference number: A22564; MUID: 8727140; PMID: 2866136

A; Title: Studies on the organization of the human apolipoprotein B 100 gene.

A; Reference number: A22605; MUID: 8727140; PMID: 3301850

A; Contente: annotation; peparin binding and disulfide bond

R; Weisgraber, K.H.; Rall Jr., S.C.
J. Biol. Chem. 252, 1109-11103, 1103-1103, 1986

A; Contente: annotation; peparin binding protein.

B; Reference number: A22605; WUID: 8720149; PMID: 3087360

A; Contente: annotation; calcium binding protein.

A; Reference number: A22605; WUID: 8720499; 1286

A; Title: Human apolipoprotein B is a calcium binding protein.

A; Reference number: A22605; WUID: 8720499; 1286

A; Title: Apolipoprotein B is a calcium binding protein.

A; Reference number: A22605; WUID: 8720499; 1286

A; Title: Human apolipoprotein B is a calcium binding protein.

A; Reference number: A22605; WUID: 8720499; 1286

A; Title: Human apolipoprotein B is a calcium binding protein.

A; Reference number: A22605; WUID: 8720499; MUID: 8720499; MUID: 8720499; MUID: 8720499; MUID: 8720499; MUID: 8720499; MUID: 8720499; MUID: 8720499; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Mesocricetus auratus (golden hamster)
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
R.Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A;Reference number: A60950, MUID:90324804; PMID:2373961
A;Recession: C60950
A,Molecule type: DNA
A;Residues: 1-269 cLAM>A;Residues: UNIPROT:060537; UNIPROT:060536
C;Superfamily: apolipoprotein B
C;Reywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apolipoprotein B-100 - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%; Score 42; DB 1; Length 4563; 90.0%; Pred. No. 12; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.0%; Score 38; DB 2
80.0%; Pred. No. 5.5;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3385 rkírkkölk 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :||| |||||
216 SRLTRKRGLK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: 137180
```

g

ઠ

ö

Gaps

ö

ö

Gaps

ö

Indels

RESULT 4

셤

ઠ

ò g

```
multiple sugar-binding periplasmic receptor chve precursor [imported] - Agrobacterium tr. (5,5pecies Agrobacterium tumefaciens C;5pecies 130-5ep-2001 #sequence_revision 30-5ep-2001 #text_change 09-Jul-2004 C;Accession: B97642 A;Accession: B97642 A;Accession: B97642 A;Almixle, G; Gattung, S; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, Science 294, Si33-2328, 2001 A; Liu, F; Wollam, C; Allinger, M.; Doughty, D.; Scott, C; Lappas, C.; Markelz, B;Aritle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumes. A;Reference number: A97359; MUID:2160851; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-354 <KUR>
A,Cross-references: UNIPROT:P25548; GB:AE007869; PIDN:AAK88091.1; PID:g15157521; GSPDB:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S17648
R;Allert, S.; Ernest, I.; Poliszczak, A.; Opperdoes, F.R.; Michels, P.A.M.
Eur. J. Biochem. 200, 19-27, 1991
A;Title: Molecular cloning and analysis of two tandemly linked genes for pyruvate kinase A;Reference number: S17648; MUID:91348039; PMID:1879424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: $17648
A;Molecule type: DNA
A;Residues: 1-499 <ALL>
A;Cross-references: UNIPROT:P30615; EMBL:X57950; NID:g10947; PIDN:CAA41018.1; PID:g10948
A;Experimental source: strain 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Pathway: glycolysis
C.Superfamily: pyruvate kinase
C.Superfamily: pyruvate kinase
C.Keywords: ATP biosynthesis; glycolysis; magnesium; metalloprotein; phosphotransferase;
F;50,212,263/Binding site: substrate phosphate (Arg. Ser. Arg) #status predicted
F;239/Active site: Lys #status predicted
F;239,333/Binding site: potassium (Gln, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Description: catalyzes the transphosphorylation of phosphoenolpyruvate and ADP to pyru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Trypanosoma brucei
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyruvate kinase (EC 2.7.1.40) isoform 2 - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S17649
R;Allert, S.; Ernest, I.; Poliszczak, A.; Opperdoes, P.R.; Michels, P.A.M.
Bur. J. Blochem. 200, 19-27, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 1; Length 499;
Pred. No. 41;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pyruvate kinase (EC 2.7.1.40) isoform 1 - Trypanosoma brucei
C;Species: Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 35; DB 2;
70.0%; Pred. No. 30;
tive 1; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Gene: AGR C_4267
A, Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                          141 TSITDKLGLK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :||| |||
141 TSITDKLGLK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||:||:
171 RLTDRRGI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLTDKRGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Genetica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sugar binding protein (imported) - Agrobacterium tumefaciens (strain C58, Dupont)

C) Species: Agrobacterium tumefaciens
C) Species: Agrobacterium tumefaciens
C) Date: 11-30an-2002 #sequence_revision 11-3an-2002 #text_change 09-Jul-2004
C) Accession: AC2865
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
RXTD, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Bter, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Accession: AC2865
A;Attus: Dreliminary
A;Molecule type: DAA
A;Residues: 1-354 aKUR,
A;Koss-references: UNIPROT:P25548; GB:AB008688; PIDN:AAL43337.1; PID:g17740831; GSPDB:GC;Genetimental source: strain C58 (Dupont)
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-193 <KUR>
A,Cross-references: UNIPROT:033773; GB:AE006641; NID:913813761; PIDN:AAK40907.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
A;Gene: hisB
C;Superfamily: imidazoleglycerol-phosphate dehydratase; imidazoleglycerol-phosphate dehy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inidazoleglycerol-phosphate dehydratase (hisB) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: D90206 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001 A;Reference number: Sulfolobus solfataricus complete genome.

A;Reference number: A99139
A;Accession: D90206
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                           Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.0%; Score 35; DB 2; Length 193; Best Local Similarity 70.0%; Pred. No. 17; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.0%; Score 35; DB 2; Length 354; Best Local Similarity 70.0%; Pred. No. 30; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                           Indels
                                                                                                                                           5
                                                                                                                                     Score 35; DB
Pred. No. 15;
1; Mismatches
A;Molecule type: DNA
A;Residues: 1-170 <HUA>
A;Cross-references: UNIPROT:P25548; GB:M30318
                                                                                                                              Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative 1
                                                                                                                                                                                                                                                                                              | :[|| |||
141 TSITDKLGLK 150
                                                                                                                                                                                                                                                            1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | ||||:|
81 TALGDKRGIK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTDKRGLK 10
| :||| |||
```

ò

ö

Gapa

ö

Gaps

us-09-823-418-8.rpr

Ŋ

ö

Gaps

ö

Length 563 1; Indels

```
Ayaricty: kinase [imported] - human herpesvirus 6 (etrain HST)
C;Species: human herpesvirus 6
Ayaricty: strain HST
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44029
C;Accession: T44029
A;Risegawa, Y; Mukkai, T; Nakano, K; Kagawa, M; Chen, J; Mori, Y; Sunagawa, T; Kaw J, Virol. 73, 8053-8063, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and A;Reference number: 222732; MUID:99412319; PMID:10482554
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T44029
A;Accession: T440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C'Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
Kyeywords: aminotransferase; lacomerase
F;2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status pred:
F;2/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       κιτυβε-rererences: UNIPROT:Q9K1P9; GB:AE002361; GB:AE002098; NID:g7225245; PIDN:AAF405
A;Experimental source: serogroup B, strain MCS8
C:Ganetian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 2; Length 563;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 2; Length 612;
Pred. No. 50;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: U69
C;Superfamily: human cytomegalovirus phosphotransferase
Score 35; DB 2
Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.0%;
nilarity 87.5%;
Conservative (
          70.0%;
                                               66.7%;
                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                      |:||||| :
422 RMTDKRGCR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 RMTDKRGCR 430
                                                                                                                                                                                                            2 RLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     224 RLTDKNGL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLTDKRGL 9
     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-612 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
A;Title: Molecular cloning and analysis of two tandemly linked genes for pyruvate kinase A;Reference number: S17648; MUID:91348039; PMID:1879424 A;Accession: S17649
                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-499 <ALL>
A; Residues: 1-499 <ALL>
A; Residues: 1-499 <ALL>
A; Expensimental source: unippose the transphosphorylation of phosphoenolpyruvate and ADP to pyru A; Pentrion: catalyzes the transphosphorylation of phosphoenolpyruvate and ADP to pyru A; Penthway: glycolysis (Superfamily: pyruvate kinase (Superfamily: pyruvate kinase (Skywords: APP biosynthesis; glycolysis; magnesium; metalloprotein; phosphotransferase; F; 50, 212, 251/Binding site: substrate phosphate (Arg, Ser, Arg) #status predicted F; 239/Active site: Lys #status predicted F; 299, 333/Binding site: potassium (Gln, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   At yearlest studing interpolations of Attaches studies of Attaches studies and interpolations of Attaches studies of Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attaches and Attac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphotransferase (EC 2.7.1.-) - human herpesvirus 6 (strain Uganda-1102)
CiSpecies: human herpesvirus 6
CiSpecies: human herpesvirus 6
CiSpecies: human herpesvirus 6
CiSpecies: human herpesvirus 6
CiSpecies: Junec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
CiAccession: E36769
Bilawrence, G.L.; Chee, M.; Craxton, M.A.; Gompels, U.A.; Honess, R.W.; Barrell, B.G.
A.Yirol. 64, 287-299, 1990
A.Title: Human herpesvirus 6 is closely related to human cytomegalovirus.
A;Reference number: A33560; MUID:90080132; PMID:2152817
A;Residues: 1-562 < LAM>A;Residues: 1-562 < LAMA>A;Residues: 1-563 < LAMA>A;Residues: 1-563 < LAMA>A;Residues: 1-563 < LAMA>A;Residues: 1-563 < LAMA>A;Residues: 1-563 < LAMA>A;Residues: 1-563 < LAMA>A;Residues: 1-563 < L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable phosphotransferase (BC 2.7.1.-) U69 [similarity] - human herpesvirus 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: human cytomegalovirus phosphotransferase C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 35; DB 2; 75.0%; Pred. No. 41; ative 2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%; Score 35; DB 66.7%; Pred. No. 46; cive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: human herpesvirus 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||||| :
421 RMTDKRGCR 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||:||:
171 RLTDRRGI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLTDKRGL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

ö

Gaps

ö

Indels

ö

Gaps

..

Search completed: December 29, 2004, 12:39:07 Job time : 11.6591 Becs

```
TISSUE-Liver;

BEDILNES-297075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,

Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=57176;
Lipoprotein.
NON TER
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                            Q7YQR5
Q7YQR5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     028473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      028473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q72600 homo sapien
Q72600 homo sapien
Q7168 glaucomys v
Q7nhs0 gloeobacter
Q7yr10 diceros bic
Q7yqms nyctimene a
Q7yqm7 pteropus hy
Q7yr04 rousettus a
Q7yr04 cousettus a
Q7yr04 cousettus a
Q7yr05 chactophrac
Q7nnf4 agouti paca
Q7nn71 hydrochoeru
Q71772 erethizon d
Q60536 mesocricetu
Q60537 mesocricetu
Q60537 mesocricetu
Q60793 rhodopseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
homo sapien
homo sapien
arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  streptomyce
giardia lam
infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gallus gall
phalanger o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6u2n6 infectious
Aaq75361 infectiou
Q616z2 thermoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7yqm9 ornithorhyn
Q7yqn0 tachyglossu
Q7tn70 dinomys bra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7yqr5 aotus vocif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             тасаса fasc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                              December 29, 2004, 12:13:11; Search time 58.4091 Seconds (without alignments) 98.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          071277
07yqn2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09kxp4
082788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q13788
P04114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7r285
                                                                                                                                                                                                                                                                                              1825181
             GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7YQRS
Q28473
Q13788
APB HUMAN
Q7ZG00
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q60536
Q60537
Q6N7G3
CAE27735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09KXP4
0827S8
Q7R285
Q6U2N6
AAQ75361
Q6L6Z2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBLCX0
Q7TN68
Q7NHS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7YR08
Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7YQM9
Q7YQN0
Q7TN70
                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D7TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27YR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27YQM8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27TN72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27YON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27YQM7
                                                                                                                                                                                                                                                                                                                                                                                                                              UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                           US-09-823-418-8
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                        1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                        Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bed
                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                      OM protein
                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                    Run on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 4 5 9 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š.
```

```
..
              Q61705 thermoprote
Bad1895 thermopro
033773 sulfolobus
Q885r4 bacteroides
Q72jp7 thermus the
Aa831069 thermus the
Q9cgm3 m mus muscu
Q9cgm3 m gmsculu
P25548 agrobacteri
Q7tn65 atherurus a
Q7tn65 trypanosoma
P30615 trypanosoma
Bad18908 thermopro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-22761261, PubMed=12878460,

Amrine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

Am new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 2255-240(2003).

EMBL; AF$48396; AAP$7352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apolipoprotein B (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45955 MW; EEFA8492157E1BDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2;
Pred. No. 7.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   596 AA
                                                                                                                                                                                                                                                                                                                                                                             414 AA
                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                HIS7 SULSO
QBA5R4
Q72JP7
AAS81069
                                                                                                                    Q9CQM3
Q91WA1
CHVE_AGRT5
                                                                                                                                                                                                             KPY1_TRYBB
KPY2_TRYBB
                Q6L705
BAD18895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actus vociferans (Spix's owl monkey).
                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                          ul-OCT-2003 (TrEMBirel, 25, Create 01-OCT-2003 (TrEMBirel, 25, Last a 01-OCT-2003 (TrEMBirel, 25, Last a Apolipoprotein B 100 (Fragment). Name-apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
NCBI_TaxID=9541;
|||| |||||
258 TRLTRKRGLK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTDKRGLK 10
```

```
SEQUENCE FROM N.A.
                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bjursell G.;
                   Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zannis V.
                OCC STATES SEED OF STATES SEED OF STATES SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED OF SEED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APB HUMAN STANDARD; PRT; 4563 AA.
P04114; O00502; Q13787;
01-NOV-1986 (Rel. 03, Last sequence update)
01-NOV-1986 (Rel. 03, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein B-48].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.; "Analysis of the human apolipoprotein B gene; complete structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
"Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 3262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Liver;
Murray R.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3262 AA; 370140 MW; 56603BC0618DD40D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  596 AA; 66757 MW; B13BBA74B25C3120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the B-74 region.";
Gene 49:29-51(1986).
BENL; M15421; AA51758.1; -.
PIN; A27850; LPHUB;
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
GO; GO:0006869; P:lipid transport; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 2;
Pred. No. 11;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 3262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87191999; PubMed=2883086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                        EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APOB protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||| ||||
2084 TRLTRKRGLK 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 TRLTRKRGLK 235
                                                                                                                                                                                                                                                                                                                                                                                    296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                       1
596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                   Lipoprotein.
NON TER
NON TER 59
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           013788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          013788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APB HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
      RTT REP REL SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET TO SET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

ACCOCCOS OD THE STAN SO OT THE STAN SO OD THE STAN SO OT THE STAN

g ð

```
SEQUENCE OF 3109-4563 FROM N.A.
MEDLINE-85300528; PubMed=2994225;
Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Evey-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
Mahley R.W., Scott J.;
"Human apolipoprotein B: structure of carboxyl-terminal domains, sites
of gene expression, and chromosomal localization.";
[10]
                                                                                                                                              MEDLINE-87016385; PubMed-3763409; Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J., Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.; "Complete cDNA and derived protein sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE-87008488; PubMed-3755943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.,
"The complete cDNA and amino acid sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86041888; PubMed=3903660; Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F., Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.; Human apolipoprotein B. identification of cDNA clones and characterization of mRNA.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
MEDLINE=86093680; Pubmed=3841204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-87041416; PubMed=3464946;
Law S.W., Grant S.W., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.
"Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
derived amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE=88003974; PubMed=3652907;
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of human apolipoprotein B cDNA.";
Nucleic Acids Res. 13:8813-8826(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 709-906 FROM N.A.
MEDLINE=65270450; PubMed=3860836;
Deeb S.S., Motullarky A.G., Alberta
"A partial cDNA clone for human apolipoprotein B.
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146 (1986)
                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 14:7501-7503 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 13:6937-6953(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 261:12918-12921(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87161758; PubMed=3030729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 3056-3159 FROM N.A.
```

```
VARIANT LEU-2739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=APOB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7Z600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-86149325; PubMed-3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kirsher S.W., McBnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87039351; PubMed=3773997;
Knott T.C., Peage R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
Levy-Wilson B., Scott J.;
"Complete protein adquance and identification of structural domains of human apolipoprotein B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Liee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L., Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.";
Nature 323:738-742(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100.";
Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
                                                                                                                                                                                                                             MEDLINE=88018019; PubMed=3659919; Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H., Silberman S.R., Cai S.-J., Dealypere J.P., Rosseneu M., Gotto A.M. Jr., Li W.-H., Chan L., "Appolipoprotein B-48 is the product of a messenger RNA with an organ-
                                                                                                   SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE-86287319; PubMed=3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.; "Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene."; Hum. Genet. 86:91-93(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT FDB GLN-3527.
MEDLINE-89098975; PubMed-2563166;
Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20143590; PubMed=10679026; Zhao Y., McCabe J.B., Vance J., Berthiaume L.G.; Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprote on B.M. a calcium binding protein.";
Biochem. Biophye. Res. Commun. 137:493-499(1986).
                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986)
                                                                apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                                                 PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Cell 11:721-734(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91071750; PubMed=1979313;
                                                                                                                                                                                                                                                                                                    specific in-frame stop codon.";
Science 238:363-366(1987).
SEQUENCE OF 1-291 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALMITOYLATION OF CYS-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 323:734-738(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALCIUM-BINDING DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT SER-4338.
                                                                                                                                                                                                                                                                                                                                             DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAINS.
```

```
VARIANTS FDB GLN-3527 AND CYS-3558.

MEDLINE=97403938; PubMed=9259199;
Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
Krampf M., Giraudet P., Junion C., Boileau C.;
"Familial ligand-defective apolipoprotein B-100: simultaneous detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=59190020; PubMed=7883971; Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.; "Familial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity."; J. Clin. Invest. 95:1225-1234(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                           VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
                                                                                                                                                                                                                                                                                                                                                                                                                                  Poirier O., Ricard S., Behague I., Souriau C., Evans A.E., Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.; "Detection of new variants in the apolipoprotein B (Apo B) gene by PCR-SSCP.",
MEDLINE=91016974; PubMed=2216805; Manan L.-S., Gavish D., Breslow J.L.; "Hanan L.-S., Gavish D., Breslow J.L.; "Sequence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C., Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth B.J., Yi Q., Nickerson D.A., Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 4563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ag(X) antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%; Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97044521; PubMed=8889592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98141125; PubMed=9490296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum. Mutat. 8:282-285(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 25, TrEMBLrel. 25, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apolipoprotein B (Including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTDKRGLK 10
                                                                                                                                          VARIANT FDB CYS-3558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND ILE-3921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2004
```

ö

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7NHS0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7NHS0
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7NHS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27YR10
             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A PAC ON THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE 
                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AXX OCC OR DIT ACK
                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment)
Glaucomys volans (Southern flying squirrel)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                                                                                                                                                                                                  Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 132;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                    4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AY086357; AAM64425.1; ... Hypothetical protein. SEQUENCE 132 AA; 14674 MW; A3698270AE88CD31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hyporhetical protein.
Arabidopsis thaliana (Mouse-ear cress).
                 GO; GO:0005319; F:lipid transporter activity; IEA. GO; GO:0006869; P:lipid transport; IEA. InterPro; IPR009454; DUF1081.
InterPro; IPR001947; Lipid transprt_N. Pfam; PF06448; DUF1081; 1. Pfam; PF06448; DUF1081; 1. Pfam; PF01347; Vitellogenin_N; 1.
                                                                                                                                                                                                                                  .;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                                                                                                Score 42; DB 2
Pred. No. 97;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.0%; Score 39; DB 70.0%; Pred. No. 9.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                            84.0%;
                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                               3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 70.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 TRIIDKRGVK 50
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=64683;
                                                                                                                                                               Lipoprotein.
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glaucomys.
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBLCX0
QBLCX0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7TN68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07TN68
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
SORBRERE
                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RXX OCC OCC DE LA LIB
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AN 121 SEQUENCE FROM N.A.

SC STRAIN=PCC 7421;

RX MEDLINE=29770464; PubMed=14621292;

RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., TBuchiya T.,

RA Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S.,

RA Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S.,

RA Kohara M., Tabata S., Racuchi C., Shimpo S.,

RA Complete genome structure of Gloeobacter violaceus PCC 7421, a

RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a

RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a

RT "Anobacterium that lacks thylakoids.";

DNA Res. 10:137-145(203)

DR GO, GO:0009058; P:Diosynthesis; IEA.

DR GO; GO:0009058; P:Diosynthesis; IEA.

DR GO; GO:0009058; P:Diosynthesis; IEA.

DR Fam: PF00534; Glyco_trans.1.

PEM: Pfam: PF00534; Glyco_trans.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
SEQUENCE FROM N.A.

MEDLINE-2761261: PubMed=12878460;

Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AX243379; AAP50767.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7YR10;
Q7YR10;
01-0CT-2003 (TEMBLE-1. 25, Created)
01-0CT-2003 (TEMBLE-1. 25, Last sequence update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-2003 (TEMBLE-1. 25, Last annotation update)
01-0CT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.0%; Score 38; DB 2; Length 421; 80.0%; Pred. No. 52; cive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%; Score 38; DB 2; Length 430; 77.8%; Pred. No. 53; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    421 421
421 AA; 46747 MW; D47B77BD4F864FD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 AA; 47641 MW; 0F8D1A8F7A38342D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Cyanobacteria, Chroococcales, Gloeobacter
NCBI_TaxID=33072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 26, C
(TrEMBLrel. 26, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G112465 protein.
OrderedLocusNames=g112465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 80.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 SŘLŤRKŘĠĽK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gloeobacter violaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||||
231 RLTDKKGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
Les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
SEQUENCE 430 AA
                                                                                                                                                                                                                                                                                                                              Lipoprotein.
NON TER
NON TER 42
SEQUENCE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (
01-MAR-2004 (
01-MAR-2004 (
```

ö

Gaps

; 0

```
Apolipoprotein B (Fragment).

Rousettus amplexicaudatus (Common rousette).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;

Pteropodinae; Rousettus.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrino-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker; apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=22761261; PubMed=12878460; Mayne R.K., Springer M.S.; Marine-Madden H., Koepfil K.-P., Wayne R.K., Springer M.S.; M.A. new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apolipoprotein B (Fragment).
Chaetophractus villoaus (South American armadillo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
                                                                                                                                                                                               76.0%; Score 38; DB 2; Length 438; 80.0%; Pred. No. 54; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                            1 1
438 438
438 AA; 48734 MW; 2BD85BCBF4E2CC41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
438 438
438 AA; 48597 MW; 41C890DEAF95C872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Last sequence update)
, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                  438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 54;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                 Local Similarity 80.0
hes 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                              281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 SRLTRKRGLK 290
                                                                                                                                                                                                                                                                     1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29080;
                                                                                                           Lipoprotein.
NON TER
NON TER
43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein.
NON TER
NON TER
SEQUENCE 438
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7YR08
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
     STTRRETES
                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolitoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AX243375; AAP50763.1; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An ew phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AF548435; AAP97391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nyctimene albiventer (Common tube-nosed fruit bat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pteropus hypomelanus (Small flying fox).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Chiroptera, Megachiroptera, Pteropodidae;
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                 Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%; Score 38; DB 2; Length 436; 80.0%; Pred. No. 54;
                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                           1 432 432
432 AA; 48171 MW; F27B7AB39604732C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                              76.0%; Score 38; DB 2;
80.0%; Pred. No. 54;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2003 (TrEMBLrel. 25, Creat
O1-OCT-2003 (TrEMBLrel. 25, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                             Query Match
Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                           :||| |||||
275 SRLTRKRGLK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||| |||||
279 SRLTRKRGLK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
436
                                                                                                                                                                                                                                                                                      1 TRLIDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pteropodinae; Pteropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=48988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein.
NON TER
NON TER
SEQUENCE 43
                                                                                                                              Lipoprotein.
                                                                                                                                           NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7YQM7
```

RESULT 10

ò a .

Gaps

ö

RESULT 11 O7YOM7

ò

```
Search completed: December 29, 2004, 12:37:36 Job time : 60.5202 secs
                                                    NON_TER
SEQUENCE
                                                                                           Query Match
                                                                                                                       Matches
          SFF
                                                                                                                                                     à
                                                                                                                                                                             셤
                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-22761261; PubMed=12878460;
Amrine-Madeen H. KoepEli K.-P., Wayne R.K., Springer M.S.;
Am new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol.

EMBL, AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                           Agouti paca (Paca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

MEDLINE=2761261; PubMed=12878460;

MEDLINE=2761261; PubMed=12878460;

MEDLINE=2761261; PubMed=12878460;

Medline Marker application of the provides compelling widence for eurherian relationships ";

Mol. Phylogenet. Evol. 225-240(2003).

EMBL; AZ43369; AAP507571; --

InterPro; IPR000871; Beta_lactamase_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Fragment)
Hydrochoerus hydrochaeris (Capybara) (Carpincho)
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Hystricognathi, Hydrochaeridae;
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                    Score 38; DB 2; Length 445;
Pred. No. 55;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; Score 38; DB 2; Length 445; 80.0%; Pred. No. 55; 1; Mismatches 1; Indels
                                                          445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                445 AA
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AX243378; AAP50766.1; -.

Lipoprotein. 1 1 1

NON TER 445 445

SEQÜENCE 445 AA; 49564 MW; 2DA5DC3ED2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                 76.0%;
                                                                                                 Query Match 76.0
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                               111 |||||
288 SRLTRKRGLK 297
                                                                                                                                                           1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 8, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                           Q7TN64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7TN71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
 STRWRE
                                                                                                                                                          ઠે
                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
Gaps
                                                                                                                                      ;
0
                                                                                                76.0%; Score 38; DB 2; Length 445; 80.0%; Pred. No. 55; tive 1; Mismatches 1; Indels
                                  1 1
445 445
445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
Lipoprotein.
NON TER
                                                                                                              Local Similarity 80.0
                                                                                                                                                                                    :||| |||||
288 SRLTRKRGLK 297
                                                                                                                                                                1 TRLIDKRGLK 10
```

ô

```
December 29, 2004, 12:10:41 ; Search time 54.9205 Seconds (without alignments) 58.786 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                    2002273
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              2002273 seqs, 358729299 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          geneseqp2003as:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_23Sep04:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geneseqp1980s:*
geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          geneseqp2002s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    geneseqp2000s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  geneseqp2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                          US-09-823-418-13
                                                                                                                                                                                                                              1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                Run on:
                                                                                                                                                                                          Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aay30694 Apo-B100	-			Abg97506 Human NOV	Abo58868 Human gen	Adk71826 Human kin	Adp29449 Human sec	Ade38441 Human pro	Adj75552 Marker ge	Apo-B1(		-		-	•		Aaw57207 Apo B 100	Aaw41261 Apolipopr	Aaw96892 ApoB-100	Abj37575 Heparin b	Aaw57208 Apo B 100	Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a
SUMMARIES	ID	Y306	AAY30695	AAY30696	ABR43240	ABG97506	AB058868	ADK71826	ADP29449	ADE38441	ADJ75552	AAY30684	AAY30683	AAY30686	AAY30682	AAY30685	AAY30687	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876
	DB	7	7	7	9	Ŋ	œ	œ	œ	7	۵	~	7	7	7	~	7	~	~	7	7	9	0	0	'n	7
	Query Match Length	0	9	6	404	548	151	311	933	984	984	10	10	10	10	10	10	11	13	15	15	20	22	22	34	36
ote	Query Match	100.0	93.2	93.2	79.5	79.5	77.3	77.3	77.3	77.3	77.3	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1
	Score	44	41	41	35		34	34	34	34	34	33.5	•	33.5	m.	ä	•	33.5		•	•	33.5	٠	•	33.5	•
	Result No.		7	3	4	2	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aaw64587 Human apo Aaw96845 Nucleic a Abb37687 Peptide # Abc\$2504 Human liv		Apolip Amino Human	Add48677 Human Pro Aao15893 Human apo Abr40253 Human ali Abu79140 Apolipopr	Adf43408 Apolipopr Adh18871 Human apo Adh18870 Human apo Ado33445 Human apo Ado33447 Human apo
AAW64587 AAW96845 ABB37687 ABG52504	AAR72704 AAR34031 ADJ57400 AAY31237	AAW41262 AAW96826 AAU98981	ADD48677 AAO15893 ABR40253 ABU79140	ADF43408 ADH18871 ADH18870 ADO33445 ADO33447
0 0 4 4	0101000	M 10 10	C 60 60	r & & & & &
37 343 343	377 377 2463	4536 4536 4560	4561 4563 4563 4563	4563 4563 4563 4563
76.1 76.1 76.1 76.1	76.1	76.1 76.1 76.1	76.1 76.1 76.1	76.1 76.1 76.1 76.1
	3333 3333 3333 3333 3333 3333 3333 3333 3333	33.55	33.5 33.5 33.5 5	33333 33333 33333 33333
26 27 29 29	3210	3334 3654	33 33 40 40	4 4 4 4 4 1 4 6 4 7

## ALIGNMENTS

RESULT 1

AMY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Claim 17; Page 57; 70pp; English. AAY30694 standard; peptide; 9 AA 98US-0077618P. 99WO-US004805. Innerarity TL, Boren JOS; (first entry) (REGC ) UNIV CALIFORNIA. WPI; 1999-551509/46. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999, Synthetic. AAY30694; 

```
1 TRLTRRGLK 9
    Sequence 9 AA;
                                                       Matches
                                                                                                                                                             RESULT 3
     g
                                                                                 ò
                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroseleroselerosis. The peptides are derived from antino acids 3358 to 3367 of apo8100. The method compounds are detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method compounds which distruct LDL-RG binding without inhibiting LDL receptor binding Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether also be used to dentify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether formation of atherosclerotic lesions. The polymucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                  ô
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                   Gabs
                                                                                                                                                                                                                                                                                                                                                                        Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                              Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                  ö
                                                                                                                        Length 9;
                                                                                                                                               Indels
                                                                                                                      100.0%; Score 44; DB 2; Lilarity 100.0%; Pred. No. 1.7e+06; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                   AAY30695 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boren JOS;
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                    σ
                                                                                                                                                                          1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-551509/46.
                                                                                                                                                                                                    1 TRLTRRGLK
                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Innerarity TL,
                                                                                              Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-1998;
                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-1999;
                                                                                                                                                                                                                                                                                                                      17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                             AAY30695;
                                                                                                                                                Matches
                                                                                                                                                                                                                                                     RESULT 2
    85888855588
                                                                                                                                                                                                 셤
                                                                                                                                                                            ò
```

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
      Score 41; DB 2; Length 9;
Pred. No. 1.7e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.2%; Score 41; DB 2; Length 9; 88.9%; Pred. No. 1.7e+06; ive 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                              AAY30696 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 57; 70pp; English.
   93.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551509/46.
Query Match
Best Local Similarity
                                                                                                                                                                                                 TRLTKRGLK
                                                                                                                                      1 TRLTRRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY30696;
```

Conservative

us-09-823-418-13.rag

```
2001US-0274849P.
2001US-0275235P.
2001US-0275579P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0276000P.
2001US-0277239P.
2001US-0277327P.
                                                                                                                                                                                 79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2002; 2002WO-US007283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-0275601P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0277338P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001US-0277791P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-0277833P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0278152P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0278894P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0279344P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0280233P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0280802P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0288148P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0294821P.
2001US-0335302P.
2001US-0338375P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2002; 2002US-00094466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                             ||:|:||:
367 TRITKRGLE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human NOVX25 protein.
                                                                                                                                                                                                                                                                     1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP
                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                            Sequence 404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200272770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2001;
14-MAR-2001;
20-MAR-2001;
20-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2001;
21-MAR-2001;
22-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2001;
27-MAR-2001;
28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001;
02-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG97506;
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                    ABG9750
  ន្តដ្ឋឧប្ដន្ឋន្ឋ
                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                        $\times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \times \
                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Becha SD;
Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC5959 to ACC59889 encode the human protein modification and maintenance molecule proteins given in ABR43240 to ABR43270, designated professed in the phink-11 (1) have cytostatic, antiatrenioselerotic, antiallergic, antinflammatory and thyromimetic activities, anti-HIV, antiallergic, antinflammatory and thyromimetic activities, and can be used in gene therapy. The Phink polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overaxpression of Phink, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AlDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid
                                                                                                                                                                                                                                                                                        Human; protein modification and maintenance molecule; PMMM; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elliott VS;
Yang J, Lu DAM;
SY, Ramkumar J, Be
AE, Hafalia AJA, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Tang YT, Ellic
Gietzen KJ, Yang
Bon TW, Lee SY, F
In UK, Kable AE, F
                                                                                                                                                                                                                                                                                                                                                                                                                   hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hawla NK, ner--
i JX, Griffin JA, Gietzem
i JX, Griffin JA, Gietzem
Duggan BM, Richardson TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 206-207; 270pp; English.
                                                                                                                      ABR43240 standard; protein; 404 AA
                                                                                                                                                                                                                                                 Human PMMM-1 protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2001; 2001US-0322196P.
21-SEP-2001; 2001US-0324134P.
26-OCT-2001; 2001US-0346198P.
02-NOV-2001; 2001US-0348198P.
09-NOV-2001; 2001US-0343887P.
16-NOV-2001; 2001US-0343445P.
28-NOV-2001; 2001US-0334145P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-2001; 2001US-0337451P, 25-JAN-2002; 2002US-0351928P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2002; 2002WO-US029221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-0366837P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chawla NK,
Li JX, Gri
||||||:|||
TRLTRKGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-354597/33.
N-PSDB; ACC59959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003025131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehr-Mason PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002;
                                                                                                                                                                                                        07-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emerling BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sprague WW,
Marquis JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infections
                                                                                                                                                               ABR43240;
                                                                                                       ABR43240
                                                                                                                           유
```

```
C compounds for effectiveness as agonist of the polypetides of inflatential ple accession for the category of the polypetides of inflatential the accession of the frager polymelotide and compounds for the inflating the accession of the frager polymelotide and compounds for the inflating the accession of the frager polymelotide and compounds for the inflating the accession of the frager polymelotide and compounds for the inflating the accession of the polymelotide and compounds for the inflating the accession of the polymelotide and compounds for the inflating the accession of the inflating the accession of the polymelotide and compounds for the inflating the accession in mention of the polymelotide and compounds for the inflating the accession in mention of the accession inflating the accession in mention of the accession in the accession in the accession in the accession in the accession in the accession in the accession in the accession in the accession in the accession accession in the accession accession in the accession accession in the accession accession and accession in the accession accession and accession accession accession and accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession accession
```

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for

Hanzel DK;

Rank DR,

Penn SG,

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

WPI; 2004-119264/12

Claim 45; SEQ ID NO 32502; 80pp; English.

surveying tissues.

```
The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or dispossing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, thippel-Lindau palsy, pollepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangisctasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, atherosclerosis, hypertension, colerosis, hammodeficiencies, HVV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and colerosis asthma, arthritis, immunodeficiencies, HVV, viral, bacterial or parasitic colerosis, properties may also be used as targets for the identification of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                    New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecules that modulate or inhibit e.g. neurogenesis, cell defferentiation, cell proliferation, haematopolesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NoVX substances for use in therapeutic or infagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present amino acid sequence represents a human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gарв
                    Tchernev VT, Malyankar UM, Gerlach VL;
turajan M, Gusev VY, Kekuda R, Pena CEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.5%; Score 35; DB 5; Length 548; 66.7%; Pred. No. 1.5e+02; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome derived single exon protein #5102.
    Vernet CA, Tchermunusen BD, Patturajan M, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABO58868 standard; protein; 151 AA.
                                                                                                                                                                                                                                                    Claim 1, Page 161; 266pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein of the invention
                                Zerhusen BD, Pa
1, Gangolli EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:|:|||:
515 TRITKRGLE 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRLTRRGLK 9
                                                                                                                                                                                                              Parkinson's disease.
                                                                                              2002-713508/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                N-PSDB; ABS78750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-2004
                    Spytek KA,
                                                    Zhong M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO58868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB058868
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or iragments, and sequences in the specification, or their complements or iragments, and sequences in the specification. The probe is a single exon probe that the fully defined in the specification. The probe is a single exon probe that children under this stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-captured acid comprising a plurality of single exon nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-captured acide above, where each of the plurality of purbles is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a wetor comprising the single exon contiguous amino acide of any of the above-mentioned amino acid exon probe cited above, and acided peptide comprising at least 8 contiguous amino acide of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an extended of selling and/or licensing single exon probes or microarray to a customer destring to measure gene expression, and a computer readable exon probes or microarray in solated antibody that binds specifically to a peptide cited above, as customer destring to measure gene expression and acid substitutions) and a customer destring to expression and acid substitutions of a customer destring to a customer destring and a database having a plurality of records to record including data on the expression of a single exon probe according to actor and analysis. The probes may be used as tools for surveying crossesion analysis. The probes may be used as tools for surveying crossesion analysis. The probes may be used as tools for surveying alternative splicing events, in detecting and characterising alternative splicing events, in detectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.3%; Score 34; DB 8; Length 151; 100.0%; Pred. No. 65; 0; Indels iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human kinase and phosphatase KPP-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK71826 standard; protein; 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 LTRRGLK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK71826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADK71826
%XCCCCCCCCCCCCCCCCCCCCCCCCCCCCX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ********
```

03-APR-2002; 2002US-00029386; 03-APR-2002; 2002US-00029386.

US2003194704-A1.

16-OCT-2003.

```
The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The polypeptide of the invention demostrates cardiovascular, antiarteriosclerotic, hypotensiave, vasotropic, antianginal, anti-HIV, antiallergic, antiathergic, antianginal, anti-HIV, antiallergic, antiatherior, nephrotropic, antigout, gastrointestinal, neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological, antitheumatic, antiparkinsonian, nootropic, antilipaemic, antiparastic, antihelmunic, antibacterial, virucide, protozoacide and funglicide activities. The kinase and phosphatase (KPP) polyuncleotides, polypeptides, agonists and antipacterial, virucide, protozoacide suppersonists and phosphatase (KPP) polyuncleotides, polypeptides, agonists and antagonists may be useful for diagnosing, treating or preventing antagonists may be useful for diagnosing, treating or preventing clasorders and viral, bacterial, fungal, parasitic, proliferative disorders and viral, bacterial, fungal, parasitic, proliferative disorders and viral, bacterial, fungal, parasitic, invention may be useful for creating transgenic animals to model human disease and during gene therapy. The current sequence is that of a human KPP protein of the invention.
human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antinflammatory; antianginal; anti-HIV; dermialergic; antiasthmatic; immunosuppressive; antitasthmatic; immunosuppressive; antitasthmatic; immunosuppressive; antitathroid; dermatcological; antidabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antithermatic; antipartisnosian; nootropic; antiparamit; hemostatic; crtostatic; antilpaemic; antiparasitic; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parasitic; protozoan; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tran UK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richardson TW, Marquis JP, Swarnakar A, Tang YT;
Emerling BM, Jin P, Wilson AD, Yue H, Gletzen KJ;
Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
Ramkumar J, Gururajan R, Tribouley CM, Chien D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3; 347pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2002; 2002US-0413910P.
27-SEP-2002; 2002US-0414296P.
11-OCT-2002; 2002US-0417821P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-2002; 2002US-0406172P.
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-2003; 2003WO-US026635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baughn MR, Richardson TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chawla NK, Ramkumar J,
Murage J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-226830/21.
N-PSDB; ADK71885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang YG,
                                                                                                                                                                                                                                                                                                                                               WO2004018641-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 311 AA;
                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becha SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang H,
```

```
Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                  ADP29449 standard; protein; 933 AA.
                                                                        Human secreted protein SEQ ID #216
                                                                                                                                                                                                              2002US-0406585P.
2002US-0406588P.
2002US-0406611P.
2002US-0406611P.
2002US-0406611P.
2002US-0406612P.
2002US-0406642P.
2002US-0406642P.
2002US-0406645P.
2002US-0406653P.
2002US-0406653P.
2002US-0406653P.
2002US-0410946P.
2002US-0410948P.
2002US-0410948P.
2002US-0410953P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-0410958P.
2002US-041093P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0411046P.
2002US-0411048P.
2002US-0411052P.
2002US-0411055P.
2002US-0411073P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0411111P.
2003US-0463700P.
                                                                                                                                                                            28-AUG-2003; 2003WO-US026780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2003US-0463716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32-MAY-2003; 2003US-0467230P
                                                     (first entry)
                                                                                                                                        WO2004035732-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                            29-AUG-2002;
                                                                                                                                                                                                                                                      29-AUG-2002;
29-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2003;
                                                                                                                                                                                                                                                                                  29-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                           17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-2002;
17-SEP-2002;
                                                     12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-2002;
                                                                                                                                                                                                                                                                                                            29-AUG-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                        17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2002;
                                                                                                                                                         29-APR-2004
                                   ADP29449;
RESULT 8
ADP29449
```

ô

Gaps

ö

Length 311;

77.3%; Score 34; DB 8; Length 311 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels

Local Similarity 100.

Best Loca Matches

ઠે

Query Match

ø

```
This invention relates to a novel method of treating a human subject having a tumourigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytostatic, antithyroid, antidiabetic or ophthalmological activity. The method is useful for treating a subject having a tumourigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostatic cancer) and, for example, Grave's disease and diabetic retinopathy. The present sequence is the amino acid sequence of the novel isolated human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic acid, by administering a modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
gene therapy; marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.3%; Score 34; DB 7; Length 984; 100.0%; Pred. No. 4.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lightcap ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marker gene related amino acid gequence SEQ ID NO:804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lescon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, SEQ ID NO 102; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ75552 standard; protein; 984 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hunter JJ, Macbeth KJ, Tsai F,
Williamson MW, Rudolph-Owen LA;
                                                                                                                                                                                                                                                                                                      13-AUG-2002; 2002US-0403046P.
22-AUG-2002; 2002US-0405155P.
27-AUG-2002; 2002US-0405155P.
25-OCT-2002; 2002US-0421195P.
12-NOV-2002; 2002US-042546P.
                                                                          2002US-0364517P.
2002US-0371075P.
2002US-0371507P.
                                                                                                                                 16-APR-2002; 2002US-0372984P
19-APR-2002; 2002US-0374194P
24-MAY-2002; 2002US-0382995P.
                                                                                                                                                                                           31-MAY-2002; 2002US-0385023P.
14-JUN-2002; 2002US-0388853P.
17-JUN-2002; 2002US-0389395P.
                                                                                                                                                                                                                                                 25-JUN-2002; 2002US-0391324P.
15-JUL-2002; 2002US-0395944P.
22-JUL-2002; 2002US-0397726P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein 1420 of the invention
                  30-JAN-2003; 2003WO-US002588
                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-2002; 2002US-0425456P
19-NOV-2002; 2002US-0427626P
10-DEC-2002; 2002US-0432122P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-646176/61.
N-PSDB; ADE38440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLTRRGL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLTRRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 984 AA;
                                                                                                               10-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ75552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumourigenic disorder, angiogenic disorder; aberrant gene expression; aberrant protein activity; cytostatic; antithyroid; antidiabetic; ophthalmological; cancer; breast cancer; colon cancer; lung cancer; prostatic cancer; Grave's disease; diabetic retinopathy; protein 1420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWES and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                       Hestir K, Beaurang PA, Behrens D;
hakota S, Haishan L, Linnemann T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.3%; Score 34; DB 8; Length 933; 100.0%; Pred. No. 4.18+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Chu K, Lee E, Heatir K, Beaur., Huang MM, Kothakota S, Haisha.
ang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1447; 428pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein 1420 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                (FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE38441 standard; protein; 984 AA.
        19-MAY-2003; 2003US-0471336P.
22-MAY-2003; 2003US-0472430P.
22-MAY-2003; 2003US-0472430P.
09-UUN-2003; 2003US-0476609P.
09-UUN-2003; 2003US-0476641P.
08-UUL-2003; 2003US-0485218P.
                                                                                                                                                                                                                                             2003US-0486960P.
2003US-0493341P.
2003US-0493370P.
2003US-0493573P.
                                                                                                                                              2003US-0485224P.
2003US-0485325P.
2003US-0486446P.
                                                                                                                                                                                                                              2003US-0486891P.
                                                                                                                                                                                                          2003US-0486480P
                                                                                                                                                                                                                                                                                                                               2003US-0493577P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||||
175 RLTRRGL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-348438/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RLTRRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 933 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003065006-A2.
                                                                                                                                              08-JUL-2003;
08-JUL-2003;
14-JUL-2003;
                                                                                                                                                                                                     14-JUL-2003;
15-JUL-2003;
15-JUL-2003;
                                                                                                                                                                                                                                                                                    08-AUG-2003;
                                                                                                                                                                                                                                                                 08-AUG-2003;
                                                                                                                                                                                                                                                                                                                             08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                              Halenbeck RF
                                                                                                                                                                                                                                                                                                                                                                                                       Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pierce K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE38441;
```

ò 셤 ô

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDE) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which medulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in a animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                               ypo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                             Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY30683 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                99WO-US004805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||| ||||
1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTR-RGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                      WO9946598-A1.
                                                                                                                                                                                                                                                                                                                                                                35-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAR-1998;
                                                                                                                                                                                                                                                                                                           16-SEP-1999
                                                                                                                                                                    Synthetic.
                                                                                  Apo-B100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY30683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
SXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present introductive pulmonary disease. The method comprises
determining the expression level of a marker gene in a biological sample
from a subject, comparing the expression level determined with the
expression level of the marker gene in a biological sample from a healthy
ce expression level of the marker gene comprises: (a) a group of
subject, and judging whether the subject has bronchial asthma or chronic
obstructive pulmonary disease. The marker gene comprises: (a) a group of
genes (S1) whose expression levels increase when respiratory epithelial
cells are stimulated with interleukin-13; or (b) a group of genes (S2)
whose expression levels decrease when respiratory epithelial
cells are stimulated with interleukin-13. Also described: (l) a reagent (l) for
testing for bronchial asthma or chronic obstructive pulmonary disease;
co treat bronchial asthma or chronic obstructive pulmonary
cc to treat bronchial asthma or chronic obstructive pulmonary
cc an animal model for bronchial asthma or chronic obstructive pulmonary
cc disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
cuthod for producing an animal model for bronchial asthma in chronic
cobstructive pulmonary disease; (6) a therapeutic agent for bronchial
cc asthma or chronic obstructive pulmonary disease, comprising for
cc amarker gene or an antisense nucleic acid corresponding to a portion of
ct marker gene or an antisense nucleic acid corresponding to a portion of
cc aprocesion of the gene through an RNAi effect or an antibody recognising
cc aprocesion of the gene through an RNAi effect or an antibody accomising
cc aprocesion of the marker gene, and (7) a by an arker gene, and than asthma or a chronic obstructive pulmonary disease, on which a
cprobe has been immobilised to assay a marker gene. (I) has respiratory
cc and antiasthmatic activities, and can be used in gene therapy. The method
is useful for testing for or screening event invention.
cc bronchial asthma or chronic obstructive pulmonary disease. The present
cc sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method of testing for bronchial asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                       Yamaya M, Kubo H, Nagai H, Izuhara K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.3%; Score 34; DB 8; Length 984; 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db c,
. 4.3e+02;
--a 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; SEQ ID NO 804; 241pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY30684 standard; peptide; 10 AA.
                                                                                                                                                                                           04-AUG-2003; 2003EP-00254857.
                                                                                                                                                                                                                                                06-AUG-2002; 2002JP-00229312
20-MAR-2003; 2003JP-00077212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOX RES INC
                                                                                                                                                                                                                                                                                                                                                                                          Ohtani N, Sugita Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 RLTRRGL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-193155/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RLTRRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 984 AA;
                          Homo sapiens.
                                                                               EP1394274-A2.
                                                                                                                                       03-MAR-2004.
```

1;

Gaps

ï

Indels

;

AAY30684;

RESULT 1: AAY30684

Query Match

ઠે 셤 Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing

98US-0077618P.

10-MAR-1998;

(REGC ) UNIV CALIFORNIA

Boren JOS;

Innerarity TL,

WPI; 1999-551509/46.

atherosclerosis.

Homo sapiens

```
Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                  Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                             AAY30686 standard, peptide, 10 AA.
                                      99WO-US004805
                                                 98US-0077618P
                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US004805,
                                                                          Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                       17-NOV-1999 (first entry)
                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                               1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                   1 TRLTR-RGLK 9
                                                                                      WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                               atherosclerosis.
                                                                                                                                                                                                                                                               Sequence 10 AA;
            WO9946598-A1
                                     05-MAR-1999;
                                                 10-MAR-1998;
                        16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                          AAY30686;
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                                                                                                                                                      윱
                                                                                                                                                                                                                                                                                                  ò
```

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which commutations. They were created to identify compounds which commutations acids 3358 to modifiate atheroselzerois. The peptides are derived from amino acids 3358 to 3357 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the compounds which medulate atheroselerosis and/or LDL-FG binding. They can also be used to identify compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether formation of atheroselerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                              Claim 17; Page 57; 70pp; English.
ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY10582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which areceptor mutations. They were created to identify compounds which andulate atherosclerosels. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to atherosclerosis. The transpanic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred, No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 57; 70pp; English.
```

```
ä
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo-B100; proteoglycan receptor mutation, atherosclerosis;
low density lipoprotein; proteoglycan; LDL, atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                   .,
;
                                                                                   76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred. No. 5.4; ive 0; Mismatches 0; Indels
                                                                                                                                                                          Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY30682 Btandard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Innerarity TL, Boren JOS;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                        TRLTRSRGLK 10
                                                                                                                                                                                                                                                     1 TRLTR-RGLK 9
                                   Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9946598-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY30682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY30682
ID AAY30
XX
XX
XX
XX
DT 17-NO
XX
XX
XX
APO-B
XX
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
XX
APO-B
APO-B
XX
APO-B
APO-B
XX
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO-B
APO
```

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which arceptor mutations. They were created to identify compounds which acceptor mutations. They were created to identify compounds which acceptor acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor and a size of a manner acceptor acceptor and a size of a manner acceptor and a size of a manner acceptor attention of a therosclerosis. The transgenic non-human animals and mammals which attention and an animal and an invivo model system for the acceptor and an acceptor and an invivo model system for the acceptor also be used to identify compounds which result in an increase in also be used to identify compounds which result in an increase in a prevent regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polymucleotides can also be acceptor and a particular food or drug composition are acceptor and a particular food or drug composition are acceptor and a particular food or drug composition acceptor acceptor and a particular food or drug composition acceptor acceptor and a particular food or drug composition acceptor acceptor and a particular food or drug composition acceptor acceptor and a particular food or drug composition acceptor acceptor and a particular food or drug composition acceptor acceptor and a particular food or drug composition acceptor acceptor and a particular food acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor acceptor
                                                                                    tifying compounds which affect binding of low density lipoprotein proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred. No. 5.4; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY30685 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                    Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRERGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTR-RGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-551509/46.
WPI; 1999-551509/46.
                                                                                                                                                                        atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-1999
                                                                           Identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY30685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PACK SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTIO
```

Claim 17; Page 57; 70pp; English.

Gaps

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which conditions activated from amino acids 3358 conditions activated from amino acids 3358 to 3367 of apoB100. The method comportses detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (FG). The method compounds unit proteoglycan (FG). The method can be used for identifying compounds which disrupt LDL-FG binding withbut inhibiting LDL receptor binding. Such compounds can be used to requere or prevent the formation of atherosclerotic lesions and prevent catherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred. No. 5.4; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 29, 2004, 12:28:50 Job time : 54.9205 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.0
Les 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLTR-RGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
8
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 8.69118 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-13 1 TRLTRRGLK 9 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Seguence:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	34	77.3	984	-	A34076	protein-tyrosine k
2	34	77.3	1099	~	AE1065	conserved hypothet
m	33.5	76.1	596	N	S32802	apolipoprotéin B -
4		76.1	4563	-	LPHUB	
2	33	75.0	189	~	B95329	probable ISRm25b t
9	33	75.0	274	N	D72044	hypothetical prote
7	33	75.0	274	~	A86581	ical
œ		75.0	368	7	A11291	glycerol dehydroge
σ	33	75.0	368	~	AG1663	
10	33	75.0	427	~	A84155	hypothetical prote
11	33	75.0	451	~	F95869	
12		75.0	514	~	F87592	cal
13	33	75.0	633	N	T05005	
14	33	75.0	871	~	T07863	~
15	32	72.7	161	N	T35260	
16	32	72.7	351	~	JC1175	
17	32	72.7	437	N	S54978	6-phosphofructokin
18	32	72.7	631	N	T29926	hypothetical prote
19	31	70.5	85	N	G81430	hypothetical prote
20	31	70.5	66	~	A87912	protein B0205.5 [i
21	31	70.5	128	N	F87342	conserved hypothet
22	31	70.5	155	~	E82452	anaerobic ribonucl
23	31	70.5	188	N	JU0451	hypothetical 21K p
24	31	70.5	188	N	159116	
25	31	ö	188	~	A29867	hypothetical 20K p
26	31	•	188	7	179500	myc protein - huma
27	31	70.5	248	7	S77172	glucose dehydrogen
28	31	٠	261	7	G87325	siroheme synthase
29	31	70.5	275	~	876916	hypothetical prote

hypothetical prote probable acyl-coen D-amino-acid oxida	D-amino-acid oxida D-amino-acid oxida D-amino-acid oxida hypothetical prote	alanine racemase {     branched-chain ami     hypothetical prote     probable cobyrinic	ABC transporter pr probable phosphogl beta-fructofuranos ribonucleoprotein malate dehydrogena
A65020 B90399 JH0185	OXPGDA S01340 JX0132 S43067	C87455 H75444 AD2219 T03545	T17948 T41375 C52332 C75418 A13372
221	4448	0000	00000
279 318 345	347 347 347 357	364 393 353	462 466 531 774
70.5	70.5	70.5 70.5 70.5	70.5 70.5 70.5 70.5
31 31	313	33131	331
31 31 32	6 8 8 8 6 4 17 0	37 38 40	4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

# ALIGNMENTS

RESULT 1

```
protein-tyrosine kinase (EC 2.7.1.112) receptor type eph 1 precursor - human NiAlternate names: receptor tyrosine kinase eph C.Species: Homo sapiens (man) c.Species: Homo sapiens (man) c.bate: 22-Oct-1999 #text_change 09-Jul-2004 C.Accession: A34076; S44280 E.Hitrai, H.; Maru, Y.; Hagiwara, K.; Nishida, J.; Takaku, F. Science 238, 1717-1720, 1987
                                                                                                                                                                                                                                                                                                       A;Title: A novel putative tyrosine kinase receptor encoded by the eph gene. A;Reference number: A34076; MUID:88070650; PMID:2825356
A;Accession: A34076
```

A; Molecule type: mRNA A; Residues: 1-984 c4HTs. A; Residues: 1-984 c4HTs. A; Residues: 1-984 c4HTs. A; Note: the sequence in GenBank entry HUMTKR, release 111.0, has the codons GCG for 398 A; Note: the sequence in GenBank entry HUMTKR, release 111.0, has the codons GCG for 398 A; Note: the sequence in GenBank entry HUMTKR, release 111.0, has the codons GCG for 398 B; Note: the sequence in GenBank entry HUMTKR, release 111.0, has the codons GCG for 398 A; Description: An EGFR/eph chimeric receptor possesses ligand stimulated tyrosine kinas: A; Reference number: 544280 A; Molecule type: mRNA A; Residues: 286-397, A', 399-580, 'QRDRAIDVDREDKLWLKPYVDLQAYEDPAQGALDF', 583, 625-984 <TUZ> C; Genetics:

A;Genec: GDB:EPHT1; EPH; EPHT
A;Cross-references: GDB:119875; OMIM:179610
A;Cross-references: GDB:119875; OMIM:179610
A;Cross-references: GDB:119875; OMIM:179610
A;Cross-references: GDB:119875; OMIM:179610
C;Kapwords: AT2-d32-d36
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein
F;1-23/Domain: signal sequence #status predicted <ATA>
F;548-568/Domain: transmembrane #status predicted <ATA>
F;630-895/Domain: protein kinase homology <AIN>
F;630-66/Region: protein kinase ATP-binding motif
F;918-984/Domain: SAM homology <ASAM>
F;5918-984/Domain: SAM homology <ASAM>
F;5918-384,414,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

ö 77.3%; Score 34; DB 1; Length 984; 100.0%; Pred. No. 90; ive 0; Mismatches 0; Indels Query Match 77,3 Best Local Similarity 100. Matches 7; Conservative

ö

Gaps

RESULT 2

AE1065 conserved hypothetical protein STY4851 [imported] - Salmonella enterica subsp. enterica C, Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi

```
A; Molecule type: mRNA
A; Residues: 1-97, 1', 99-328,'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-
A; Residues: 1-97,'I', 99-328,'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-
A; Residues: 1-97,'I', 99-328,'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-
A; Residues: 1-97,'I', 910-610,'NID: 9178803; PIDN: AAA35549.1; PID: 9178804
A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
R; Procter, A.A.; Hardman, D.A.; Sato, R.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; HI
Proc. Natl. Acad. Sci. U.S.A. 83, 5578-5682, 1986
A; Reference number: A24320; MUID: 86287319; PMID: 3461454
A; Reference number: A24320; MUID: 86287319; PMID: 3461454
A; Residues: 1-97,'I', 99-617,'A', 619-941,'YYIWSLPPKPY', 951-1138,'PTGRLPNCFSNGLICYSLWLHSFQEI
A; Residues: 1-97,'I', 99-617,'A', 619-941,'YYIWSLPPKPY', 951-1138,'PTGRLPNCFSNGLICYSLWLHSFQEI
A; Residues: 1-97,'I', 99-617,'A', 619-941,'YYIWSLPPKPY', 951-1138,'PTGRLPNCFSNGLICYSLWLHSFQEI
A; Law, S.W.; Lackner, R.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor, Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A; Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A; Reference number: A24684; MUID: 86094221; PMID: 301697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 485-617, 74, 619-1044 <LAZ>
A; Residues: 485-617, 74, 619-1044 <LAZ>
A; Crocker, A: A: GB: MIZ480; NID: 9178791; PIDN: AAAS1751.1; PID: 9178792
R; Procter, A: A: Hardman, D: A: Schilling, J W.; Miller, J: Appleby, V.; Chen, G.C.; Kil-
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr
A; Reference number: A94088; WUID: 86149325; PMID: 3513177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1282-2731,2742-3290,'L',3292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180,
A; Cross-references: GB:MI5421; ND:9178817; PIDN:AAA51758.1; PD:9178818
R; Hardman, D.A.; Protter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana
Biochemistry 26, 5478-5486, 1987
A; Title: Structural comparison of human apolipoproteins B-48 and B-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 709-791, 'SSSKKAASHGCPHSAGD', 810-906 <DEE>
A; Cross-references: GB:K03175; NID:g178821, PIDN:AAA51759.1; PID:g178822
R; Carlsson, P.; Darnfors, C.; Olofsson, S.O.; Bjursell, G.
A; Title: Analysis of the human apolipoprotein B gene; complete structure of
A; Reference number: A91565; MUID:87191999; PMID:2883086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-291 < PRO>
A; Cross-treferences: GB: Mal2681; NID:g178797; PIDN:AAA51753.1; PID:g178798
B; Deeb, S. S.; Mctulsky, A. G.; Albers, J. J.
Proc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
A; Title: A partial CDNA clone for human apoliprotein B.
A; Reference number: A25774; MUID:85270450; PMID:3860836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A24684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nontains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: B-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
CiSpecies: Dec-1987 #sequence = revision 28-Dec-1987 #text change 09-Jul-2004
CiSpecies: A27650; A25679; A25673; A25267; A25266; A24320; A24684; A2317; A266
A452; I61909; I55510; I39474; I39469; I84624; I37179; PS0058
Riudwdg, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scc
BN 6, 363-372, 1987
A; Ttile: DNA sequence of the human apolipoprotein B gene.
A; Recence number: A27850; MUD:88003974; PMID:3652907
A; Molecule type: DNA
A; Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78473; UNIPROT:Q9UNNO; UNIE
BNBO J. S, 3495-3507, 1986
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A; Reference number: A21058; MUD:8716778; PMID:3030729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  applipoprotein B - crab-eating macaque (fragment)

C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Accession: 332802
C;Accession: 332802
C;Accession: S32802
B;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.W.; Hunt, C.E.; Marotti, K.R.; Melchic Biochim. Biophys. Acta 1086, 3328.34, 1991
A;Title: Apo B metabolism in the cynomigus monkey: evidence for post-transcriptional re A;Accession: 832802; Mulb:92075708; PMID:1742325
A;Accession: 832802
A;Kstatus: preliminary
A;Molecule type: mRNA
A;Rsiduas: 1-59 cAPA>
A;Rsiduas: 1-59 cAPA>
A;Cross-references: UNIPROF:Q28473; EMBL:X15737; NID:938047; PIDN:CAA33755.1; PID:993012
                             CjAccession: AE1065
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE1065
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AL513382; PIDN: CAD06970,1; PID: 916505611; GSPDB: GN00176
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.3%; Score 34; DB 2; Length 109
100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.5; DB
Pred. No. 71;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein B-100 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.1%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 77.3
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 90.(
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 TRLTRKRGLK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTR-RGLK 9
                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-1099 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTRRGLK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: STY4851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

reg

```
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free sn R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Kreterence number: A22006
A, Molecule type: protein
A, Residues: 873-892'(K', 894-896 < LE1>
A, Accession: A22006
A, Molecule type: protein
A, Residues: 873-892'(K', 894-896 < LE1>
A, Accession: B22006
A, Molecule type: protein
A, Residues: 3113, 'L', 3115-3130,' R', 3132-3133,' P', 3135-3136,' R' < LE2>
A, Accession: B22006
A, Molecule type: protein
A, Residues: 3113, 'L', 3115-3130,' R', 3132-3133,' P', 3135-3136,' R' < LE2>
R, Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C., J. Biol. Chem. 261, 15564-15367, 1986
A, Title: Structure of the human apolipoprotein B gene.
A, Reference number: A92564; MUID:87057153; PMID:2946672
A, Title: Studies on the organization of the human apolipoprotein B 100 gene.
R, Magener, R.; Pitzner, R.; Stoffel, W.
Biol. Chem. Bope-Seyler 368, 419-425, 1987
A, Title: Annotation; gene structure
R, Weisgraber, R.H. Rall Ur., S.C.
J. Biol. Chem. 262, 11097-11103, 1987
A, Title: Human apolipoprotein B-100 heparin-binding sites.
A, Reference number: A92605; MUID:87280197; PMID:3301860
A, Contents: annotation; heparin binding and disulfide bond
R, Asseternce number: A92605; MUID:87280197; PMID:307360
A, Title: Apolipoprotein B is a calcium binding protein.
A, Title: Apolipoprotein B is a calcium binding protein.
A, Title: Apolipoprotein B is a calcium binding protein.
A, Title: Apolipoprotein B is a calcium binding protein.
A, Title: Apolipoprotein B is a calcium binding protein.
A, Title: Apolipoprotein B is a calcium binding protein.
A, Title: Apolipoprotein B is a calcium binding protein.
A, Title: Molecular Agolipoprotein B cDNA.
A, Title: Molecular cloning of human apolipoprotein B cDNA.
A, Title: Molecular cloning of human apolipoprotein B cDNA.
A, Title: Molecular cloning of human apolipoprotein B cDNA.
A, Title: Molecular cloning of human apolipoprotein B cDNA.
A, Title: Molecular cloning of human apolipoprotein B cDNA.
A, Title: Molecular cloning of human apolipoprotein B cDNA.
A, Title: Afolipoprotein B contains cloning of the contains con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable ISRm25b transposase [imported] - Sinorhizobium meliloti (strain 1021) magaplasm. C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Spacession: B95329
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilor
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: B95329
A;Status: preliminary
A;Actus: preliminary
A;Actus: preliminary
A;Actus: preliminary
A;Actus: preliminary
A;Coulocule type: DNA
A;Cross-references: UNIPROT:Q92ZEB; GB:AE006469; PIDN:AAK65196.1; PID:g14523642; GSPDB:A;Cross-references: Unipropried as a;Experimental source: strain 1021, megaplasmid pSyma
A;Experimental source: strain 1021, megaplasmid pSyma
A;Experimental source: strain 1021, megaplasmid pSyma
B;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
                                                 А;Accession: A35783
A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33.5; DB 1;
Pred. No. 4.7e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.1
Best Local Similarity 90.0
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3385 rkirkkkcik 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Reference number: A40133; MUID:88018019; PMID:365919
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 940133
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Accession: 94013
A, Acces
                                            Ajaccession: A29671
Ajaccession: A29671
Ajaccession: A29671
Ajaccession: A29671
Ajaccession: A29671
Ajaccession: A29671
Ajaccession: 1671-2323, PWW, 2327-2352, 'H', 2354-2398 cHRR>
Ajaccession: 1671-2323, 'PWW, 2327-2352, 'H', 2354-2398 cHRR>
Ajaccession: 1671-2323, 'PWW, 2327-2352, 'H', 2354-2398 cHRP>
Ajaccession: A2987
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2988
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A2572
Ajaccession: A24738
Ajaccession: A24738
Ajaccession: A24738
Ajaccession: A24738
Ajaccession: A24738
Ajaccession: A24738
Ajaccession: A24738
Ajaccession: A24738
Ajaccession: A24738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39
A; Cross-references: GB:M12413; NID:g178735; PIDN:AAA51742.1; PID:g178736
R; Chen, S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cai
Science 238, 363-366, 1987
A; Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
A; Reference number: A40133; MUID:88018019; PMID:3659919
number: A29671; MUID:88050832; PMID:3676265
```

```
A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0724
C;Superfamily: Chlamydia pneumoniae hypothetical protein CPn0724
                                                                                                                                                                                                                                                                                                                                                                                           |: |||||:
41 TKATRRGLR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 THLERRGLK 35
                                                                                                                                                                                                                                                                                                                                               1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: AG1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein CD0022 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR NyAlternate names: hypothetical protein CPn074
CiSpecies: Chlamydophila pneumoniae, Chlamydia pneumoniae
CiDate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
CiAccession: D72044; C81621
Rikalana, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Recession: D72044
A; Status: preliminary
A; Moccession: D7204
A; Status: preliminary
A; Moccession: D7204
A; Status: preliminary
A; Moccession: D7204
A; Status: preliminary
A; Moccession: D7204
A; Status: preliminary
A; Moccession: C81092711; GB:AE001653; GB:AE001363; NID:G4377017; PIDN:AAD1886
A; Cross-references: UNIPROT:O92711; GB:AE001653; GB:AE001363; NID:G4377017; PIDN:AAD1886
A; Cross-references: UNIPROT:O92711; GB:AE001653; GB:AE001363; NID:G43377017; PIDN:AAD1886
A; Cross-references: UNIPROT:O92711; GB:AE001653; GB:AE001363; NID:G43377017; PIDN:AAD1886
A; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, A; Reference number: Agilc91
A; Reference number: Agilc0; MUID:20150255; PMID:10684935
A; Reference number: Agilc0; MUID:20150255; PMID:10684935
                      Χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apportetical protein CPj0724 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86581
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Status: preliminary
A;Status: preliminary
A;Status: Dreliminary
A;Residues: 1-274 <STO>
A;Cross-references: UNIPROT:Q92711; GB:BA000008; NID:g8979096; PIDN:BAA98931.1; GSFDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <REA>
A;Residues: 1-274 <REA>
A;Cross-references: GB:AE002166; GB:AE002161; NID:G7188959; PIDN:AAF37918.1; PID:G718896
A;Experimental source: strain AR39, HL cells
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A§6039; MUID:21368234; PMID:11474104 A;Contents: annotation C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CPn0724; CP0022
C;Superfamily: Chlamydia pneumoniae hypothetical protein CPn0724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
75.0%; Score 33; DB 2; Length 274;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                  Length 189
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                       75.0%; Score 33; DB 75.0%; Pred. No. 31; ive 2; Mismatches
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||||||:
106 KLTRRGLR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: |||||:
41 TKATRRGLR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLTRRGLK 9
                                                                                                                                                                             A;Gene: SMa0998
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
Al1291

Glycerol dehydrogenase homolog lmo1737 [imported] - Listeria monocytogenes (strain EGD-e-CySpecies Listeria monocytogenes (strain EGD-e-CySpecies Listeria monocytogenes (strain EGD-e-CySpecies)

C;Accession: Al1291 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004

C;Accession: Al1291 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004

C;Accession: Al1291 L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.

D.; Jones, L.M.; Karst, U.

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Malok, C.; Schlueter, T.; Simoss, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycerol dehydrogenase homolog lin1848 [imported] - Listeria innocua (strain Clip11262) c. Species: Listeria innocua c. Species: Listeria innocua c. Species: Listeria innocua c. Species: Listeria innocua c. Species: Listeria innocua c. Species: Listeria innocua c. Species: Listeria innocua c. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. Species: C. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-368 <GLA>
A;Cross-references: UNIPROT:08Y6F0; GB:NC_003210; PIDN:CAC99815.1; PID:g16411191; GSPDB..
A;Experimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1.368 <GLA>
A;Cross-references: UNIPROT:Q92AS1; GB:AL592022; PIDN:CAC97079.1; PID:gL6414350; GSPDB:(
A;Experimental source: strain Clip11262
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: 1mo1737
C;Superfamily: Glycerol dehydrogenase; lactaldehyde reductase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: lin1848
C;Superfamily: Glycerol dehydrogenase; lactaldehyde reductase homology
                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
            Score 33; DB 2; Length 274; Pred. No. 44; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 2; Length 368;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.0%; Score 33; DB 2; Best Local Similarity 77.8%; Pred. No. 58; Matches 7; Conservative 0; Mismatches 2
Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%;
```

us-09-823-418-13.rpr

```
hypotherical protein CC2774 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: F8752
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B; Laub, M.T.; DeBoy, R.T.; Dodson, K.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; WUID:21173698; PMID:11259647
A;Accession: F87592
A;Accession: preliminary
A;Residues: 1-514 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9A4Q6; GB:AE005673; NID:g13424372; PIDN:AAK24738.1; GSPDB:c
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T19P19.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05005
R;Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15394
A;Accession: T05005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable polyprotein - pineapple retrotransposon deal (fragment)

C;Species: Ananas comesus (pineapple)

C;Species: Ananas comesus (pineapple)

C;Accession: 107863

R;Thomson, K.G.; Thomas, J.E.; Dietzgen, R.G.

R;Thomson, K.G.; Thomas, J.E.; Dietzgen, R.G.

R;Thomson, K.G.; Thomas, J.E.; Dietzgen, R.G.

R;Thomson, R.G.; Thomas, J.E.; Dietzgen, R.G.

R;Thomson, K.G.; Thomas, J.E.; Dietzgen, R.G.

R;Thomson, K.G.; Thomas, J.E.; Dietzgen, R.G.

R;Thomson, R.G.; Thomas, J.E.; Dietzgen, R.G.

A;Title: Retrotransposon-like sequences integrated into the genome of pineapple, Ananas

A;Reference number: Z16184; MUID:98418625; PMID:9747853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-871 <THO>
A;Cross-references: UNIPROT:064892; EMBL:Y12432; NID:g2995404; PIDN:CAA73042.1; PID:g29:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A,Residues: 1-633 <BEV>
A;Residues: 1-633 <BEV>
A;Cross-references: UNIPROT:065655; EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19P19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 2;
Pred. No. 78;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 2
Pred. No. 95;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 4
A;Introns: 385/1; 448/1; 498/3
A;Note: T19P19.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 75.0
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 TELKRRĞLK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 kirtrkcik 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CC2774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T05005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable ABC transporter sugar-binding protein SWb20231 [imported] - Sinorhizobium melill CiSpecies: Sinorhizobium meliloti
CiSpecies: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
CiAccession: F95669
Rifinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95669
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-451 <KUR>
A;Residues: 1-451 <KUR>
A;Residues: 1-51 <KUR>
A;Cross-references: UNIPROT:092WV7; GB:AL591985; PIDN:CAC48622.1; PID:G15140094; GSPDB:GA;Experimental source: strain 1021, megaplasmid pSymB
A;Cross-references: UNIPROT:092WV7; GB:AL591985; PIDN:CAC48622.1; PID:G15140094; GSPDB:GA;Experimental source: strain 1021, megaplasmid pSymB
A;Cross-references: UNIPROT:092WV7; GB:AL591985; PIDN:CAC48622.1; PID:G15140094; GSPDB:GA;Experimental source: strain 1021, megaplasmid pSymB
A;Cross-references: UNIPROT: Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kahn, M.L.; Kahn, M.L.; Kahn, M.L.; Weiller, P.; Weille: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference unmber: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                          CjAccession: A84155
R; Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira
Nucleic Acida Res. 28, 4317-4317, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID: 20512582; PMID: 11058132
A; Accession: A84155
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-427 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9KSP7; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB077 A;Experimental source: strain C-125 C;Genetics: A;Gene: BH4041
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                           hypothetical protein BH4041 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
   Gaps
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 451; 70;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
   ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 2
Pred. No. 66;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 33; DB 87.5%; Pred. No. 70; iive 0; Mismatches
   Mismatches
   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.0
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 87.5
Matches 7; Conservative
   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:|:|| |
TRITKRGRK 347
                                                                                                                27 THLERRGLK 35
                                                         TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTLTRRGL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: SMb20231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
   Matches
                                                            ઠે
                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

A; Mobile element: retrotransposon deal

```
hypothetical protein SC5F2A.18 - Streptomyces coelicolor C,5pecies: Streptomyces coelicolor C,5pecies: Streptomyces coelicolor C,5pecies: Streptomyces coelicolor C,5pecies: Streptomyces coelicolor C,5pecies: OS-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004 C;Accession: T35260
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. A;Oliver, K.; Harris, Data Library, April 1999
A;Reference number: Z21573
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accession: T35260
A;Accessi
                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                             Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                       ,
0
Query Match
Pest Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
72.7%; Score 32; DB 2; Length 161;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: December 29, 2004, 12:39:08 Job time : 9.69318 secs
                                                                                                                                                                                                                                                                                                                           272 TRLTHKGVK 280
                                                                                                                                                                                                                                  1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||:
144 RLTRRGI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 RLTRRGL 8
                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

O8v6f0 listeria

Q9rdb7 streptomyce Q82cw6 streptomyce Q82cw6 streptomyce Q75tw9 bacillus fi Q75tm6 bacillus fi Q75tm1 bacillus al Q75tx1 bacillus ha Q75tx3 bacillus ha Q75tx6 bacillus ha Q75tx7 bacillus ha Q75tx7 bacillus ha Q75tx7 bacillus ha Q75tx7 bacillus ha

423 AA

7

```
STRAIMERLEGIA:

MEDLINE-22753791, PubMed=12730200;

MEDLINE-22753791, PubMed=12730200;

MEDLINE-22753791, PubMed=12730200;

MEDLINE-22753791, PubMed=12730200;

M. Garchar R., Hauettermann J., Fetzner S.;

M. Gane Cluster of Arthrobacter ilicis R.61a Involved in the Degradation of Arthrobacter ilicis R.61a Involved in the Degradation of Quinaldine 4-oxidase qoxLMS Genes.";

M. Expression of the Quinaldine 4-oxidase qoxLMS Genes.";

M. J. Biol. Chem. 278:27483-27494 (2003).

M. Diol. Chem. 278:27483-27494 (2003).

M. Diol. Chem. 278:27483-27494 (2003).

M. GO; GO:0006215; F:transporter activity; IEA.

M. GO; GO:0006215; F:transporter activity; IEA.

M. GO; GO:0006810; P:transporter activity; IEA.

M. GO; GO:0006810; P:transporter activity; IEA.

M. MILE-PPO: IPROOTINE, MES.

M. ROSITE; PSSO860; MRS; 1.

M. SEQUENCE 423 AA, 43696 MW; BB11CBADA85DF241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Arthrobacter ilicis.
Bacteria; Actinobacteria; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=43665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical cytosolic protein.
Name=FNV0795;
Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                              01-007-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 2;
Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                     ALIGNMENTS
0816F0
09RDB7
09RDB7
075TW6
075TW6
075TW6
075TW1
075TX3
075TX3
075TX3
075TX6
075TX6
075TX6
075TX7
075TX6
075TX7
075TX7
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   Putative transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 84.1%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
 |||||::|||
207 TRLTKQGLK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=209882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] -
SEQUENCE FROM N.A.
STRAIN=ATCC 49256;
 75.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
77.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusobacterium.
   Q7P2I3
Q7P2I3;
                                                                                                                                                                                                                                                                                                                                    Q7WSQ9
                                                                                                                                                                                                                                                                                                    RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
   Q7WSQ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7P2I3
                                                                                                                                                                                                                                                                                                                                                   RANK OCCOSTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 098nd4 rhizobium 1
073uw5 mycobacteri
Aas06799 mycobacte
092ze8 rhizobium m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q87wz9 pseudomonas
Q8phw2 xanthomonas
Q71yr1 listeria mo
Aat04533 listeria
Q92as1 listeria in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8n1e6 homo sapien
Q740b8 mycobacteri
Aa803750 mycobacte
095916 homo sapien
Q97121 neurospora
Q871b9 neurospora
Q871b9 rhizobium 1
P21709 homo sapien
Q82021 salmonella
060359 yarrowia li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macaca fasc
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusobacteri
gallus gall
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27wsg9 arthrobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actus vocif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fusobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           (without alignments)
98.508 Million cell updates/sec
                                                                                                          December 29, 2004, 12:13:11 ; Search time 52.5682 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O7p2i3
O8reil
O8qhi6
O8bid8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7yqr5
Q28473
Q13788
P04114
Q7z600
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAC4 HUMAN
Q98HM9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COBB_RHILO
EPA1_HUMAN
Q8ZOZI
                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FXLE MOUSE
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FXLE HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         013788
APB HUMAN
Q7Z600
Q98ND4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q73UW5
AAS05799
Q92ZE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q740<u>B</u>8
AAS03750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q71YT1
AAT04533
Q92AS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7P2I3
Q8REI1
Q8QHI6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7RZ12
Q871B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7YQR5
Q28473
                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             060359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287WZ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 PHW2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29Z7II
                                                                                                                                                                                                                                                                                                                                                                                                                                                            UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                         US-09-823-418-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
                                                                                                                                                                                                     TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
596
3262
4563
4563
184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              976
1099
1906
                               Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                          Seguence:
                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                            .
ПО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š.
                                                                                                            Run
```

ô

Gaps

ö

0; Indels

503 AA

Length 423;

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                        TER
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FXLE MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C STRAINATICE 25586;
X MEDLINE-21886394; PubMed=11889109;
K Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., A Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., A Battacharyya A., Battman A., Gardner W., Grechkin G., Zhu L., A Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Genome sequence and analysis of the oral bacterium Fusobacterium or nucleatum strain ATCC 25586.";
T "Genome sequence and analysis of the oral bacterium Fusobacterium or nucleatum strain ATCC 25586.";
T "Babli ABO10616; ALDS317.1; -..
RMBL; ABO10616; ALDS317.1; -..
RMBL; Complete proteome; Hypothetical protein.
Complete Forteome; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N., Submitted (JAN-2003) to the EWBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lykidis A.,
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                             Score 36; DB 2; Length 503;
Pred. No. 49;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 506;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                              preliminary data.
EMBL; AABF01000083; EAA23797.1; -.
Hypochetical protein.
SEQUENCE 503 AA; 57362 MW; 70DE5CADE118516C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 2;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical cytosolic protein.
OrderedLocusNames=FN1121;
                                                                                                                                                                                                                                           81.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       126 řŘĽEŘŘGIK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRLERRGIK 134
                                                                                                                                                                                                                                                                                                                            1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTRRGLK 9
                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002
01-JUN-2003
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=PPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBREIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8REI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBOHI6
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8REI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8QHI6
      8 X Y Z C C C Z Y Y Y Y
                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCORDANCE OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
RN 113
RC SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Breast tumor, and Heart;
RX MEDLINE=CS7BL/6J; TISSUE=Breast tumor, and Heart;
RX MEDLINE=CS154683; PubMed=L12466651; DOI=10.1038/nature01266;
RA Nikaido I., Osato N., Saito R., Adachi J., Bono H., Kondoo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Baldarelli R., Anapin A., Matuda H., Batalov S., Beisel K.W.
Baldarelli R., Arangin A., Reltcher C.P., Forrest A., Gough J.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Gough J.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Maglott D.K., Maltafa L., Marchiomi L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA RA RA RA T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Setou M., Shimada K.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Shiraki T., Waki K., Kawai J., Alaawa T., Konh M., Kagawa T.,
RA Shiraki T., Waki K., Kawai J., Alaawa T., Konh M., Kagawa T.,
RA Shiraki T., Waki K., Sasaki D., Shinagawa A.,
RA Yasunishi A., Soshino M., Waterston R., Shinagawa A.,
RA Yasunishi A., Soshino M., Waterston R., Shinagawa A.,
RA Yasunishi A., Soshino M., Waterston R., Rakawa T., Konh M.,
RA Yasunishi A., Soshino M., Waterston R., Shinagawa A.,
RA Yasunishi A., Soshino M., Waterston R., Shinagawa A.,
RA Yasunishi A., Soshino M., Waterston R., Shinagawa A.,
RA Yasunishi A., Soshino M., Waterston R., Lichi H., Ka Rai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birney B., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FXLE_MOUSE STANDARD;
PRT; 400 AA.

98BLD6; QRSH7; Q8VDT7; Q922NS;
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
F-box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, Musinae, M
                                                                                                                                                                                       Das T., Purkayastha Mukherjee C., D'Angelo J., Weir M.;
"A conserved F-box gene with unusual transcript localization.";
Dev. Genes Evol. 212:134-140(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Das T.K., Purkayastha-Mukherjee C., D'Angelo J., Weir M.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AA467464; AAL75968.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR007611; LRR.
Fiam, PF00560; LRR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 AA; 20629 MW; 21702832DA5CE865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.5%; Score 35; DB 66.7%; Pred. No. 27; ive 3; Mismatches
[1]
SEQUENCE FROM N.A.
MEDLINE=21972450; Pubmed=11976951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Fbx114; Synonyms=Ppa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:|:|||:
161 TRITKRGLE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
```

ô

```
DOMAIN
                                                                                              FXLE HUMAN
                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mutting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           -> F (in Ref. 2; AAH21329).
E0B297E4B4F83C22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB
Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Übl cor
F-box.
LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR0089995; LRR cys.
InterPro; IPR008945; Skp1_Skp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AK084506; BAC39201.1; -. BMBL; BC006913; AAH06913.1; -. BMBL; BC0201329; AAH21329.1; -. BMBL; AF467463; AAL75967.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; FALSE I
Leucine-rich repeat; Repeat; Ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:2141676; Fbx114.
InterPro; IPR001810; F-box.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00646; F-box; 1.
Pfam; PF00560; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
```

ö

Gaps

ö

0; Indels

Pred. No. 63; 3; Mismatches

Conservative

```
RC TISSUE-Lung;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachung;

RA Altachung;

RA Altachung R.D., Collins F.S., Wagner L.H., Derge J.G.,

RA Altschung R.D., Reingold E.A., Grouse L.H., Derge J.G.,

Altachung S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bromstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rahes J., Helton B., Ketteman M., Greorigues S., Sanchez A.,

Rahes J., Helton B., Ketteman M., Greorigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schountz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

Rodriguez A.C., Grimwood J., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              05-UUL-2004 (Rel. 44, Created)
05-UUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
R-box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).
-1- SIMILARITY: Contains 1 F-box domain.
-1- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMARY, SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; FALSE NEG.
Leucine-rich repeat; Repeat; Ubl conjugation pathway.
                                                                                                                                                                     418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F-box.
LRR 1.
LRR 2.
LRR 3.
LRR 4.
                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC028132; AAH28132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001810; F-box.
InterPro; IPR001611; IRR.
InterPro; IPR007089; IRR_cys.
Pfam; PF00646; F-box; 1.
Pfam; PF00560; IRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:28624; FBXL14
                                                                                                                                                                     STANDARD;
                         367 TRITKRGLE 375
1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
170
203
254
                                                                                                                                                                                                                                                                                                                                           Name=FBXL14;
                                                                                                                                                                     FXLE HUMAN OBN1E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
```

us-09-823-418-13.rup

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                          Pearce A.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the small GTPase superfamily.
                                                                                                                                                                                                Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Ras-related C3 botulinum toxin substrate 4 (p21-Rac4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 AA; 21383 MW; 09CSDFE64C8E6053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                       192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 47;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL022576; -; NOT_ANNOTATED_CDS. HSSP; P15154; 1HH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC: 31113; RAC4.
InterPro; IPR00180; GTPase_Rho.
InterPro; IPR01806; Ras trinsfrung.
InterPro; IPR00525; Small_GTP.
Pfam; PF00071; Ras; 1.
PRINTS; PR00449; RASTRNSFRNNG.
SMART; SM0174; RHO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
M112796 protein.
OrderedLocusNames=m112796;
Rhizobium loti (Mesorhizobium loti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.3%;
                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
             243 TRLTRRG 249
                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 LTRKGLK 166
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LTRRGLK 9
                                                                                                                                                                                                                                  NCBI TaxID=9606;
                                                                                 RAC4_HUMAN
095916;
                                                                                                                                                                        Name=RAC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                   RAC4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98HM9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q98HM9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
098HM9
1D 098HM1
AC 090CM
DT 01-0CT
DT 01-UD
DE M11279
GN 071279
                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      Li L., Bannantine J., Zhang Q., Amonsin'A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017232; AAS03750.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 581 AA, 61736 MW, 408204895CB496RD CPC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                    Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteriles; Corymbacterineae; Mycobacterineae; Mycobacterium, Mycobacterium avium complex (MAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017232, AAS03750.1; -.
Hypothetical protein.
SEQUENCE 581 AA, 61736 MW, 4082D4B95CB496B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                         79.5%; Score 35; DB 1; Length 418; 66.7%; Pred. No. 66; 11ve 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.5%; Score 35; DB 2; Length 581; 100.0%; Pred. No. 95; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 581;
                                5779961C8177779F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               581 AA; 61736 MW; 4082D4B95CB496B0 CRC64;
                                                                                                                                                                                                                              0740B8;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein
orderedLocusNames=MAP1433C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AASO3750;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                          581 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
79.5%; Score 35; DB 2
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
 LRR 5.
LRR 6.
                                                                                                                                                                                                                       PRT;
                             45886 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium paratuberculosis.
                                        Query Match
Beet Local Similarity 66.70,
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                               ||:|:|||
367 TRITKRGLE 375
                                                                                                                1 TRLTRRGLK 9
331 3
357 3
418 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 TRLTRRG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTRRG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=k10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRLTRRG 7
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=k10;
               REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS03750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAP1433C
 REPEAT
                                                                                                                                                                                                                   Q740B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                   Q740B8
                                                                                                                                                                                                                                 à
                                                                                                                                          g
```

ઠે 셤 ò

ö

Gape

ö

ö

```
"The Genome Sequence of the Filamentous Fungus Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.v.
6; Conservative
                                                                                                                                                                                                                                              Local Similarity 75.0
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Related to oxygenase.
Name=B8G12.280;
                                                                                                                                                                                                                                                                                                                  |:|||||:
63 RITRRGLR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|||||:
63 RITRRGLR 70
                                                                                                                                                                                                                                                                                              2 RLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHILO
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 098KP1;
                                                                                                                                                                                                                                                                                                                                                                                                         0871B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COBB_RHILO
                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
Q871B9
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COBB
                                                                                                                                                                                                                                                                                                                                                                                                                         SUBBREE
                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gradin-CR74A;

A Galagan J. E., Calvo S. E., Borkovich K.A., Selker E.U., Read N.D.,

Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,

Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,

A Cui D., Ianakiev P., Federsen D., Nelson M., Washburne M.,

Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,

A Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,

Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

A Kamyssells M., Maucell E., Bielhe C., Rudd S., Frishman D.,

Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,

Cogoni C., Macino G., Catchealde D., Li W., Pratt R.J., Osmani S.A.,

DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,

Yarden O., Plamann M., Seiler S., Dunlag J., Voelker R.,

Yarden O., Plamann M., Seiler S., Dunlag J., Freitag M.,

A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,

Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
                                                                                                     Kaneko T., Nakamura Y., Sato S., Asamizu B., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";
                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.3%; Score 34; DB 2; Length 321; 100.0%; Pred. No. 82; o; Indels iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 AA; 34893 MW; C6FB1DA0CC1D73D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 7:331-338(2000).
EMBL; AP003000; BAB49837.1; -.
GO; GO:0016787; F:hydrolase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                              MEDLINE=21082930; PubMed=11214968;
                                                                          STRAIN=MAFF303099;
MEDLINE=21082936; PubMed=11214974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR004843; M-pesterase.
Pfam; PF00419; Metallophos; 1.
Complete proteome.
SEQUENCE 321 AA; 34893 MW; C6F
              Phyllobacteriaceae; Mesorhizobium
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||||
289 RLTRRGL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLTRRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicted protein.
                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=NCU07194.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7RZ12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          쉱
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Schulte U., Aign V., Mannhaupt G.; Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
Nature 0:0-0(2003).
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.3%; Score 34; DB 2; Length 378; 75.0%; Pred. No. 98; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.3%; Score 34; DB 2; Length 369; 75.0%; Pred. No. 96; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German Neurospora genome project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX294027; CAD71088.1; -.
GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006725; P:aromatic compound metabolism; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                                            Preliminary data.

EMBL, ABRACHOROTZI, EAA28183.1, -...
GO; GO:0006497; F:moncoxygenase activity; IEA.
GO; GO:0006725; P:aromatic compound metabolism; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPRO0073; F:lav moncoxygenase.
InterPro; IPRO03042; Rng_mnoxygenase.
PERm; PRO1360; Moncoxygenase; 1.
PRINTS; PRO1420; RNGMNOXGNASE.
SEQUENCE 369 AA; 40627 NW; D53DE9368557BE47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 AA; 41711 MW; 405EB2FB76BCA5A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Cobyrinic acid A,C-diamide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000733; Flav monooxygnse.
InterPro; IPR003042; Rng mnoxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01360; Monooxygenase; 1. PRINTS; PR00420; RNGMNOXGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                   Res. 77:31-38(2000).

FINCTION: Responsible for the amidation of carboxylic groups at FUNCTION: Responsible for the amidation of carboxylic groups at Dostiton A and C of either cobyrinic acid or hydrogenobrynic acid. NH(2) groups are provided by glutamine, and one molecule of ATP is hydrogenolyzed for each amidation (By similarity).

FATHWAY: Cobalamin biosynthesis.

SIMILARITY: Belongs to the cobB/cobQ family. CobB subfamily.
                                                                             STRAINMARF20309;
MEDLINE-210809;
MEDLINE-2108230; PubMed=11214968;
MEDLINE-2108230; PubMed=11214968;
MEDLINE-2108230; PubMed=11214968;
Matanabe A., Ideauwa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88070650; PubMed=2825356;
Hirai H., Maru Y., Hagiwara K., Nishida J., Takaku F.;
"A novel putative tyrosine kinase receptor encoded by the eph gene.";
Science 238:1717-1720(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPA1 HUMAN STANDARD; PRT, 976 AA.
P21709; Q15405;
01-MAY-1991 (Rel. 18, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ephrin type-A receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EPH).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
 Name=cobB; OrderedLocusNames=mlr1387;
Marizoblum loti (Mesorhizoblum loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizoblum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.3%; Score 34; DB 1; Length 439; 100.0%; Pred. No. 1.2e+02; .ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRRAMS; TIGRO0379; cobB; 1.
Cobalamin biosynthesis; Complete proteome.
SEQUENCE 439 AA; 45879 MW; DCFB9F997D2948B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
MEDLINE=99299440; PubMed=10369740;
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF01656, CbiA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||||
28 LTRRGLK 34
                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
Search completed: December 29, 2004, 12:37:38
Job time : 54.6793 secs
        Q8Z0Z1; Q7C4Y0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                        InterPro; IPR001245; TYT_pkinase.

InterPro; IPR001245; TYT_pkinase.

InterPro; IPR001245; TYT_pkinase.

InterPro; IPR001246; TYT_pkinase.

InterPro; IPR001426; TXase_receptorV.

Ream; PP001041; Ephrinase; 1.

Pram; PP001049; TYRKINASE.

ProDom; PD001049; TYRKINASE.

ProDom; PD001049; TYRKINASE.

ProDom; PD001049; TYRKINASE.

ProDom; PD001049; TYRKINASE.

PRODOM; PD00149; Ephrinase; 1.

RMART; SM00615; Ephrinase; 1.

SMART; SM00615; Ephrinase; 1.

SMART; SM00619; TYRC; 1.

PROSITE; PS001107; PROTEIN KINASE ATP; 1.

PROSITE; PS001107; PROTEIN KINASE TYR; 1.

PROSITE; PS001107; PROTEIN KINASE TYR; 1.

PROSITE; PS001107; PROTEIN KINASE TYR; 1.

PROSITE; PS001107; PROTEIN KINASE TYR; 1.

PROSITE; PS001107; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN KINASE TYR; 1.

PROSITE; PS001109; PROTEIN TYR KIN V 2; 1.

PROSITE; PS001109; PROTEIN TYR KIN V 2; 1.

PROSITE; PS001109; PROTEIN TYR KIN V 2; 1.

PROSITE; PROSITE; PS001109; PROTEIN TYR KIN V 2; 1.

PROSITE; PROSITE; PS001109; PROTEIN TYR KIN V 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | (Pocential) | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphotyrosine (by autocatalysis) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphotyrosine (by autocatalysis) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 By similarity.
Phosphotyrosine (by autocatalysis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
Phosphotyrosine (by autocatalysis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDZ-binding motif (Potential).
ATP (By similarity).
ATP (By similarity).
By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.3%; Score 34; DB 1; Length 976; 100.0%; Pred. No. 2.8e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephrin type-A receptor 1. Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
Cys-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibronectin type-III 1. Fibronectin type-III 2. Protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
InterPro; IPR008957; FN III-like.
InterPro; IPR008979; Gal bind like.
InterPro; IPR000719; Prot_kinase.
                                                                 IPR001660; SAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RLTRRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569
1191
132
624
624
630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781
                                              InterPro; InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
DOMAIN
SOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4OD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
      ઠ
```

PRT; 1099 AA.

PRELIMINARY;

Q8Z0Z1 RESULT 15

175 RLTRRGL 181

В

```
ö
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MIDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
Charle J. Janes G. James K.D., Thomson N.R., Pakran J., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Parrar J., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica servovar Typhi CT18";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIR=TY2 / Arcc 700931;
MEDLINE=22531367;
PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.3%; Score 34; DB 2; Length 1099; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 185:2330-2337 (2003).

EMBL, AL627283; CAD06970.1; -.

EMBL, AR016849; AAO71983.1; -.

COMDIATE DECEMBLY HYPOCHELICAL PROCESS.

SEQUENCE 1099 AA; 125223 MW; 6131DD4E8ABSF6A5 CRC64;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein STY4851.
OrderedocusNames=STY4851, t4545;
Salmonella typhi.
                                                                                                                                                                                                                                               Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 LTRRGLK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=601;
```

```
(without alignments)
58.786 Million cell updates/sec
                                                                                                                              December 29, 2004, 12:10:41 ; Search time 54.9205 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                     2002273
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                       2002273 segs, 358729299 residues
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                  US-09-823-418-14
                                                                                                                                                                                                                                                              1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp20018:\* geneseqp20028:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* A\_Geneseq\_23Sep04:\* geneseqp2004s:\* Database

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Aay30695 Apo-B100 Aay30694 Apo-B100 Aay30696 Apo-B100 Abc43240 Human PWM Abg97506 Human NOV Aag40845 Zea mays Add47506 Thermococ Add30649 Xanthomon Abu48780 Protein e Aar59286 GAP Protein e Aay30689 Apo-B100 Aay30689 Apo-B100 Aay30689 Apo-B100 Aay30689 Apo-B100 Aay41681 Apolipopr Aaw41861 Apolipopr Aaw41861 Apolipopr Aaw41861 Apolipopr Aaw41861 Apolipopr Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57207 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Aaw57209 Apo B 100 Protein e GAP prote Apo-B100 Apo-B100 Apo B bin Apo B bin Human apo Nucleic a Peptide # Apo B 100 Apo B 100 Aaw96845 Nucleic a Abb37687 Peptide # Abg52504 Human liv Nucleic a Description AAY30696 ABR43240 ABG97506 AAG40845 ADN47506 ADG30649 ABU48780 AAK59926 AAY30689 AAY30688 AAW57205 AAW57207 ABJ37575 AAW57208 AAW57209 AAW96845 ABB37687 ABG52504 AAW96892 AAW41261 AAE14541 4AW64587 В Length Query Match 1 Score Result Š

377 2 AAR72704 377 2 AAR727403 3923 2 AAR31237 4536 2 AAW6826 4560 5 AAW6826 4561 7 ADD4677 4561 5 ABR40253 4563 6 ABR40253 4563 6 ABR40253 4563 6 ABR40253 4563 6 ABR40253 4563 8 ADH18870 4563 8 ADH38870 4563 8 ADH3871 4563 8 ANTO699		Aay30699 Apo-B100 Aay30697 Apo-B100 Aae12587 Pseudomon
011033333310066322 4224333333310066322	AAR72704 AAR34031 AAY31237 AAW11262 AAW12626 AAW186816 AAD18893 AAD1893 ABK40253 ABU79140 ADH18871 ADH18871 ADH18871 ADH18871 ADH18871 ADH18871 ADH18871 ADH18871	AAY30699 AAY30697 AAE12587
	77 mm 9 9 0 1 mm mm mm mm m m m m m m m m m m m m	410
		0.00
		777
00000000000000000000000000000000000000		933
	0 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4. 4. 4. E. 4. 2.

# ALIGNMENTS

Apo-B100; proteoglycan receptor mutation, atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Claim 17; Page 57; 70pp; English. \$ AAY30695 standard; peptide; 9 99WO-US004805 98US-0077618P Boren JOS; (REGC ) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 16-SEP-1999 Synthetic AAY30695; RESULT 1 AAY30695 

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method comprises detecting compounds which affect without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which activity of atherosclerosis, and in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

N

ô

Gарв

ö

Score 41; DB 2; Length 9; Pred. No. 1.7e+06; 1; Mismatches 0; Indels

93.2%; 88.9%;

Query Match Best Local Similarity

Sequence 9 AA;

g

8; Conservative

Matches

σ

1 TRLTKRGLK

8 셤

us-09-823-418-14.rag

```
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                      ö
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                          Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                 Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                     ö
                                                                                                    Query Match 100.0%; Score 44; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                              AAY30694 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0077618P
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                  |||||||||
TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-551509/46.
                                                                                                                                                    TRLTKRGLK
                                                                                Sequence 9 AA;
                                                                                                                                                                                                                                                                            17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                            WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1999.
                                                                                                                                                                                                                                                      AAY30694;
                                                                                                                                                                                                                                                                                                                          Apo-B100;
                                                                                                                                                                                                        RESULT
 8888888888
                                                                                                                                                                                                                                          ò
                                                                                                                                                                     셤
```

Apo-B100; proteoglycan receptor mutation, atherosclerosis, low density lipoprotein; proteoglycan; LDL, atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation.

Synthetic. Homo sapiens. WO9946598-A1 99WO-US004805. 98US-0077618P.

05-MAR-1999; 10-MAR-1998;

16-SEP-1999.

Innerarity TL, Boren JOS;

WPI; 1999-551509/46.

(REGC ) UNIV CALIFORNIA

AAY30696 standard; peptide; 9 AA.

RESULT 3 AAY30696 ID AAY3

17-NOV-1999 (first entry)

AAY30696;

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which method computed at the peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the compounds which modulate atherosclerosis and/or LDL-PG binding. They can be used to identify compounds which result in an increase in a particular food or drug composition tends to etimulate or inhibit the formation of atherosclerosic aparticular food or drug composition tends to etimulate or inhibit the commation of atherosclerosic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 2; Length 9;
Pred. No. 1.7e+06;
2; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
```

AAY30582-Y30700 represent apo-Blo0 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which which are method comprises detecting compounds which affect to 3367 of apoBlo0. The method comprises detecting compounds which affect can be used for identifying compounds which fisciple. FG binding without inhibiting IDL receptor binding. Such compounds can be used to atherosclerosis. The transgenic non-human animals and mammals which express human apo-Blo0 can be used as an in vivo model system for the express human apo-Blo0 can be used as an in vivo model system for the express human apo-Blo0 can be used as an in vivo model system for the compounds which medulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal

1 TRLTKRGLK 9

ò

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing

Claim 17; Page 57; 70pp; English.

atherosclerosis.

```
antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becha SD;
Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC5959 to ACC59889 encode the human protein modification and maintenance molecule proteins given in ABR43240 to ABR43270, designated Professor antianteriosclerotic, antianteonormulant, nootropic, neuroprotective, carebroprotective, anti-HIV, antiallergic, antinflammatory and thyromimetic activities, and can be used in gene therapy. The PWMM polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of PWMM, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntingron's disease, stroke), immune/inflammatory (e.g. allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid
                                                                                                                                                                                                                                      Human; protein modification and maintenance molecule; PMMM; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elliott VS;
Yang J, Lu DAM;
SY, Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chawla NK, Warren BA, Tang YT, Ell:
Li JX, Griffin JA, Gietzen KJ, Yang
Duggan BM, Richardson TW, Lee SY,
M, Swarnakar A, Tran UK, Kable AE,
                                                                                                                                                                                                                                                                                                                                         hypothyroidism; Cushing's syndrome; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 206-207; 270pp; English.
                                                                                                    ABR43240 standard; protein; 404 AA
                                                                                                                                                                                                     Human PMMM-1 protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20010S-0324134P
20010S-0327233P
20010S-034369B-
20010S-034868PP
20010S-0332423P
20010S-033423P
20010S-033423P
20010S-033423P
20010S-033423P
20010S-033423P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-2002; 2002WO-US029221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-0366837P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                     (first entry)
                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-354597/33.
TRLTRKGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ACC59959
                                                                                                                                                                                                                                                                                                                                                                                                          WO2003025131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehr-Mason PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-2001;
02-NOV-2001;
09-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emerling BM,
                                                                                                                                                                     07-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sprague WW,
Marquis JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections.
                                                                                                                                     ABR43240;
                     셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain; obseity; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; scleroderma; heemophilia; diabetes; pancreatitis; autoimmune disease; sathma; arthritis; immundeficiency; HIV; viral infection; neurogenesis; bacterial infection; paraaitic infection; quaft-versus-host disease; coll differentiation; cell proliferation; haematopoiesis; wound healing;
                compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polypucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein
PMMM. The PMMMs or their fragments are useful in screening
                                                                                                                                                                                       Gaps
                                                                                    interactions, drug-target interactions, and gene expression profiles
                                                                                                                                                                                         ö
                                                                                                                                                       6; Length 404;
                                                                                                                                                                                         0; Indels
                                                                                                                                                     86.4%; Score 38; DB 77.8%; Pred. No. 20; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                ABG97506 standard; protein; 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001; 200105-0274849F

12-MAR-2001; 200105-027525F

13-MAR-2001; 200105-0275601P

14-MAR-2001; 200105-0275601P

14-MAR-2001; 200105-0275000P

20-MAR-2001; 200105-0277239P

20-MAR-2001; 200105-0277338P

21-MAR-2001; 200105-0277338P

22-MAR-2001; 200105-027739P

23-MAR-2001; 200105-027739P

24-MAR-2001; 200105-027934F

27-MAR-2001; 200105-027934F

28-MAR-2001; 200105-027933P

29-MAR-2001; 200105-027933P

20-MAR-2001; 200105-027933P

21-MAR-2001; 200105-027933P

21-MAR-2001; 200105-027933P

21-MAR-2001; 200105-028082P

21-MAR-2001; 200105-028082P

21-MAR-2001; 200105-028082P

21-MAR-2001; 200105-028082P

21-MAR-2001; 200105-028082P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2002; 2002WO-US007283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-2002; 2002US-00094466
                                                                                                                                   Ouery Match
Best Local Similarity 77.00,
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                         367 TRITKRGLE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human NOVX25 protein.
                                                                                                                                                                                                                         1 TRLTKRGLK 9
                                                                                                                      Sequence 404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200272770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                ABG97506;
                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                 ABG97506
 8888888
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                  ò
```

(CURA-) CURAGEN CORP

```
99US-0128234P.
99US-0128714P.
99US-0130077P.
99US-0130449P.
99US-0130449P.
     99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126784P.
99US-0126785P.
                                                                                                                                                                                                                                   990S-0132484P

990S-0132486P

990S-0132486P

990S-0134256P

990S-0134218

990S-013421P

990S-013421P

990S-013421P

990S-0134221P

990S-0134221P

990S-0134228

990S-013522P

990S-013522P

990S-013522P

990S-013522P

990S-013622P

990S-013622P

990S-013622P

990S-013722P

990S-013722P

990S-013722P

990S-013722P

990S-013722P

990S-013952P

990S-013965P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0139458P

990S-0140838P

990S-0140838P

990S-0140838P

990S-0140838P

990S-0140838P

990S-0140838P
                                                                                                                                                                                               99US-0131449P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0142390P.
99US-0142803P.
99US-0142920P.
99US-0142977P.
                                                                                                                                                                                                                          99US-0132407P
                05-MAR-1999;
09-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
116-APR-1999;
21-APR-1999;
21-APR-1999;
                                                                                                                                                                               23-APR-1999;
28-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                     04-MAY-1999;
05-MAY-1999;
                                                                                                                                                                                                                           30-APR-1999;
                                                                                                                                                                                                                                                                 06-MAY-1999;
                                                                                                                                                                                                                                                                              06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1999;
09-JUL-1999;
12-JUL-1999;
                                                                                                                                                                                                                                                                                                                      14-MAY-1999
                                                                                                                                                                                                                                                                                                                                    14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                              14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                        18-MAY-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NDD-91
     The present invention relates to a new polypeptide (NOVX). The NOVX colypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, confederably a NOVX-associated disorder. The NOVX nucleic acids, or preferably a NOVX-associated disorder. The NOVX nucleic acids, or dispeptides and antibodies are useful for treating, preventing or dispensing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau Syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palay, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxiactelsopaly, coherentality, inflammatory bowel disease, atherosclerosis, hypertension, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, atherosclerosis, hypertension, scleroforma, hemophilia, diabetes, pancreatitis, autoimmune disease, infections, or graft-versus-host disease. The nucleic acids and scleroforman, any also be used as targets for the identification of small complements, in gene thorapy, in generation of antibodies that bind differentiation, cell proliferation, hematopoiesis, wound healing and cimmunospecifically to NOVX substances for use in therapeutic or anglogenesis, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present amino acid sequence represents a human NOVX notes in the invanrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                       New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
            Spytek KA, Vernet CA, Tchernev VT, Malyankar UM, Gerlach VL,
Li L, Zerhusen BD, Patturajan M, Gusev VY, Kekuda R, Pena CEA,
Zhong M, Gangolli EA, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.4%; Score 38; DB 5; Length 548; 77.8%; Pred. No. 27; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays protein fragment SEQ ID NO: 50735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG40845 standard; protein; 146 AA.
                                                                                                                                                                        Claim 1; Page 161; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000; 2000EP-00301439,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.4
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|||||:
515 TRITKRGLE 523
                                                                 WPI; 2002-713508/77.
N-PSDB; ABS78750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG40845;
```

à

```
R 13-JUL-1999; 99US-0141542P.

R 14-JUL-1999; 99US-0144624P.

R 15-JUL-1999; 99US-0144624P.

R 15-JUL-1999; 99US-014468P.

R 19-JUL-1999; 99US-0144131P.

R 19-JUL-1999; 99US-0144131P.

R 20-JUL-1999; 99US-0144131P.

R 20-JUL-1999; 99US-0144131P.

R 21-JUL-1999; 99US-0144131P.

R 21-JUL-1999; 99US-0144131P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-014519P.

R 22-JUL-1999; 99US-015519P.

R 22-RUS-1999; 99US-015519P.

R 22-RUS-1999; 99US-015519P.

R 23-RUS-1999; 99US
```

```
gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermococcus kodakaraensis KOD1 protein sequence SeqID1384.
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 87.5%; Score 35; DB 3; Length 146; 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN47506 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NISC-) JAPAN SCI & TECHNOLOGY
99US-0157117P.
99US-015753P.
99US-0158029P.
99US-0158029P.
99US-0158232P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159313P.
99US-0159313P.
99US-0159634P.
99US-0159634P.
99US-016041P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016098P.
                                                                                                                                                                                                                                                                                             99US-0161405P.
99US-0161406P.
99US-0161359P.
99US-0161361P.
99US-0161920P.
99US-0161932P.
99US-0161932P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2003; 2003WO-IB003597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-AUG-2002; 2002JP-00319011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermococcus kodakaraensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imanaka T, Atomi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||||||
44 RFTKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004022736-A1
 04-0CT-1999

06-0CT-1999

08-0CT-1999

13-0CT-1999

13-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

12-0CT-1999

21-0CT-1999

22-0CT-1999

22-0CT-1999

22-0CT-1999

22-0CT-1999

22-0CT-1999

22-0CT-1999

23-0CT-1999

24-0CT-1999

25-0CT-1999

26-0CT-1999

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADN47506;
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
ADN47506
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
```

ö

9

ö

Claim 8; SEQ ID NO 6; 145pp; English.

```
This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least a sequence, providing a vector that contains a transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly contains a discussion of a game in the genome of an organism, which is applicable in the genome of a pane in the genome of an organism, which is applicable in cutython of a game in the genome of an organism, which is applicable in the genome of an organism, which is applicable in cutying gene structure and functions as well as enzyme activities of inspection, molecular biology and immunology, with this method, the disruption of a gene at an arbitrary position in a genome can be achieved disruption of a gene at an arbitrary position in a genome can be achieved the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this per mined electronic format directly from NIPO at the invention of the printed specification, but was obtained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the
                                             Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas axonopodis pv citri plant pathology-related XAC3136 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas microorganism; plant; pathology; bacterial pest; Xac; Xcc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 238; 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quaggio RB, Reinach FDC, F
ML, Setubal JC, Furlan LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 8
Pred. No. 78;
1; Mismatches
                                                                                                                                            Claim 9; SEQ ID NO 1384; 598pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG30649 standard, protein, 335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas axonopodis pv. citri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 77.3%;
Local Similarity 77.8%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-2003; 2003WO-BR000060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-2002; 2002US-0374620P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silva ACR, Farah SC,
Oliveira JCF, De Laia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rkirkidik 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTKRGLK 9
  WPI; 2004-257583/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-865444/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADG30648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003089647-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG30649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG30649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g o
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         유
```

Gaps ; 0

1; Indels

New nucleic acid molecule from a Xanthomonas microorganism, useful in determining the presence of Xanthomonas bacteria in a sample.

Ferro JA;

```
The invention relates to a novel isolated nucleic acid molecule from a Manthomonas microorganism where the nucleic acid molecule is associated with pathogenicity caused by the Xanthomonas microorganism, or its variant, that causes reduced or enhanced pathogenicity. The nucleic acid che invention may be useful in detecting the presence of Xanthomonas bacteria in a sample, as well as in plant pathology, for example, for acaded by bacterial pests. The current sequence is that of the Xanthomonas axonopodis pv. citri (Xac) plant pathology related XAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the 611 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any the 6213 antigense semisores given in the anadification when
                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                   Length 335;
                                                                                                                                                                                                                                                                                 1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #34307.
                                                                                                                                                                                                                                                Score 34; DB 7; I
Pred. No. 1.1e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 76704; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          ABU48780 standard; protein; 840 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malone C,
Carr GJ,
                                                                                                                                                                                                                                            77.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.87
Trans 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                 ||| :||||
TRLLERGLK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ureaplasma urealyticum.
                                                                                                                                                                                                                                                                                                              1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-029926/02.
N-PSDB; ACA52650.
                                                                                                                                                                                                               Sequence 335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200277183-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                             294
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU48780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                              ABU48780
ઠે
                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
```

```
proliferation, of the activity of a gale in an operon required to proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibite cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the to which each of the strains is present in a cultier acids required for organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational datiscovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the present sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neurofibromatosis type 1 (NP1)-GAP related domain (GRD) mutant clones NP201 (Given in AAR59221) and NP204 (AAR59922) show strong suppression activity for RAS7Valls, and inhibit v-Ras-induced transformation in mammalian cells. The mutation sites of these proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ras; GTPase activating protein; GAP; GAP related domain; GRD; RAS2; v-Ras; heat shock; neurofibromatosis type 1; NF1.
proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blocking Ras-induced effects on a cell - by introducing a GTPase activating protein to the cell, used esp. in treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.3%; Score 34; DB 6; Length 840; 87.5%; Pred. No. 2.9e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 63-72; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR59926 standard; protein; 3079 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US000198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-00004824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaziro Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744 RLTKRGAK 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-249216/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAP protein Ira2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 840 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9416069-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakafuku M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
22-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR59926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method compounds which disrupt LDL-PG binding withbut inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                         ö
were located in one of the most conserved regions of GRD. These sites were compared with those of other GRD family proteins, yeast Ira2 (AAR59926) and Ira1 (AAR59931), human GAP (AAR5994) and Schizosaccharomyces pombe Gap1 (AAR59925). (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                         ö
                                                                                                                                                    Length 3079;
                                                                                                                                                                                       0; Indels
                                                                                                                                                  77.3%; Score 34; DB 2; Le
100.0%; Pred. No. 1.2e+03;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       AAY30689 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0077618P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                              3029 ŘĽŤKŘĠĽ 3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-551509/46.
                                                                                                                                                                                                                          2 RLTKRGL 8
                                                                           correct PN field.)
                                                                                                               Sequence 3079 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innerarity TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9946598-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo-B100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                              AAY30689;
                                                                                                                                                    Query Match
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                      AAY30689
ID AAY3
                                                                                                                                                                                                                                                          g
   88888888
                                                                                                                                                                                                                            8
```

Seguence 10 AA;

ω

```
Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 52; 73pp; English.
                                                                                                                                                Apo B binding site peptide 2.
                                                                                                                                                                                                                                                                                                                                                                        (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                   Halbert GW, Owens MD,
1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-230637/20.
                                                                                                                       03-AUG-1998
                                                                                                                                                                                                                                                            WO9813385-A2
                                                                                                                                                                                                                                                                                                                 25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                            27-SEP-1996;
                                                                                                                                                                                                                                                                                        02-APR-1998.
                                                                                                                                                                                                                                  Synthetic.
                                                                                            AAW57205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                    AAW57205
                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which computate atherosals. They were created to identify compounds which computate atherosals. The peptides are derived from amino acids 3388 to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding with proteoglycan (PG). The method compounds to the transpend or atherosal-croats. The transpend on human animals and mammals which express human apo-B100 can be used an in vivo model system for the express human apo-B100 can be used an in vivo model system for the express human apo-B100 can be used an in vivo model system for the express human apo-B100 can be used and in vivo assay methods for identifying also be used to identify compounds which result in an increase in the appartantal food or drug composition tends to stimulate or inhibit the formation of atherosales. Thus the assays may be used to determine whether formation of atherosales in an animal or reducing the severity of atherosales in an animal or mammal
                                    1;
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                 Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                   Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                    1,
       DB 2; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred. No. 3.6; cive 0; Mismatches 0; Indels
                                0; Indels
    Score 33.5; DB
Pred. No. 3.6;
0; Mismatches
                                                                                                                                                   AAY30688 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Page 57; 70pp; English.
  76.18;
                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US004805.
                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0077618P.
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Innerarity TL, Boren JOS;
Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA.
                                                                                 1 TRLTDKRGLK 10
                                                       1 TRLT-KRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                           17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                     05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                 WO9946598-A1
                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1999
                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                AAY30688;
                                                                                                                          RESULT 12
                                                                                                                                         AAY30688
                                                                                                                                                                  a
```

ö

Baillie

97WO-GB002610. 96GB-00020153

(first entry)

```
The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that Las at least 1 binding site for an apo B protein receptor and at least 1 invention. The LDL particle of secribed in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-articles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media especially as growth supplements. Non-naturally occurring, ceceptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.1%; Score 33.5; DB 2; Length 11; 90.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TRLTRKRGLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLT-KRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57207
ID AAWF
XX
AC AAW!
XX
DT 03-1
```

1;

Gaps

7

1 TRLT-KRGLK 9

à

prothrombinase complex.

Synthetic. Homo sapiens WO9743311-A1

```
The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (DDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete app B sequence, which is large and tends to aggregate, to provide binding
                                                                                            Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-coagulant, apolipoprotein B-100, apoB-100, metastatic spread, thromboplastin-mediated process, cancer, inhibitor, blood coagulation, anglogenesis, cellular differentiation, apoptosis, KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.5; DB 2; Length 13;
Pred. No. 4.7;
0; Mismatches 0; Indels
                               Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                          /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Owens MD, Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96GB-00020153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.1%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 90.0
المالية والمالية والمالية والمالية والمالية والمالية والمالية والمالية والمالية والمالية والمالية والمالية وا
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 TRLTRKRGLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLT-KRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9813385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Halbert GW,
                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW41261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW41261
ID AAW4
XX AC AAW4
XX 19-h
XX XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
XX AAW5
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apo8-100). IL-KAQ-XI-KKONKARNE-XZ-T-ZZ (I) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids ca); Z2 = the C terminus of the peptide are used for simultaneous, ca ... Compositions containing the peptide are used for simultaneous, ca ... Compositions containing the peptide are used for simultaneous, compositions containing the peptide are used for simultaneous, compositions containing the peptide are used for simultaneous, compositions or sequential treatment of cancer, particularly to prevent or reduce blood coagulation (e.g. processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, callular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits active as such or as part of a 98-aa peptide, inhibits active and the surface of thromboplastin and of platelets by thrombin. It blinds to the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15 AA;
```

(UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.

Bruckdorfer KR, Ettelaie C;

WPI; 1998-008798/01.

96GB-00009702 97WO-GB001255

09-MAY-1997; 09-MAY-1996;

20-NOV-1997

1;

Gaps

7;

0; Indels

0; Mismatches

9; Conservative

Local Similarity

Query Match Best Local S Matches σ

1 TRLT-KRGLK

Search completed: December 29, 2004, 12:28:51

Job time : 55.9205 secs

1 rkirkkick 10

셤

Score 33.5; DB 2; Length 15; Pred. No. 5.5;

76.1%; 90.0%;

Me 28 sept.

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 8.69118 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-14 44 1 TRLTKRGLK 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	hypothetical prote	hypothetical prote	protein B0205.5 [i	glucose dehydrogen	DNA topoisomerase	probable GTPase-ac	apolipoprotein B -	apolipoprotein B-1	nucleoside diphosp	ribosomal protein	amino acid permeas	hypothetical prote		lymphotactin precu		spermidine/putresc	peroxisomal assemb	lytB protein - The	hypothetical prote		D-amino-acid oxida	D-amino-acid oxida	D-amino-acid oxida	coproporphyrinogen	hypothetical prote	unknown protein F5	branched-chain ami	hypothetical prote	
SUMMARIES		A84155	T29926	A87912	877172	F82937	RGBY12	S32802	LPHUB	A11315	R3KW13	S39733	T05005	S51368	ETHUL	140170	G70179	S27422	A72253	T50120	JH0185	OXPGDA	S01340	JX0132	A98030	B95164	E96835	H75444	AG1977	B86875
	DB	2	7	~	~	7	-	~	Н	~	Н	~	~	~	-	~	~	~	ď	N	-	-		-	~	~	N	N	~	N
	Length	427	631	66	248	840	3079	296	4563	147	151	470	633	800	114	257	263	271	275	306	345	347	347	347	376	376	389	393	454	625
d	Query Match	81.8	79.5		77.3	77.3	77.3	76.1	76.1	75.0	75.0	75.0	75.0	75.0	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7	72.7
	Score		35	34	34	34	34	33.5	ë.	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
	Result No.		7	n	4	S	9	7	89	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable polyprote myosin - Acetabula	hypothetical prote lymphotactin precu probable diphtheri	hypothetical prote alanine racemase [	hypothetical prote ABC transporter pr	dihydrolipoamide d hypothetical prote	hypothetical prote Ras-binding protei	hypothetical prote probable sulfur me	protein AC7.2 [imp
T07863 A59251	G81430 ETMSL C72769	T29841 C87455	AI2180 T17948	T44424 S18210	T25684 T42998	T30947 T38932	A88684
0.01	2 4 8	0 0	0 0	0 0	0 0	0 0	0
871 1145	85 114 180	232 364	378 462	474	485 559	572 605	613
72.7	70.5	70.5	70.5	70.5	70.5	70.5	70.5
32	4 4 4 6 8 8	31	31	31	333	31	31
30 31	2 2 2 2 2 3 4	32 36	37 38	39 40	4 4 2	4 4 8 4	45

# ALIGNMENTS

hypotherical protein BH4041 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Date: 01-6c-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004
C;Accession: A84155
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: A84155
A;Accession: A84155
A;Accession: A84155
A;Accession: A84155
A;Accession: A84155
A;Accession: A84155
C;Generics: UNIPROT:Q9K5P7; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07
A;Experimental source: strain C-125
C;Generics:
A;Gene: BH4041

Gaps ; 0 Length 427; 1; Indels 81.8%; Score 36; DB 2; 77.8%; Pred. No. 15; iive 1; Mismatches Query Match
Best Local Similarity 77.8
Matches 7; Conservative

ö

1 TRLTKRGLK 9 δ g

339 TRITKRGRK 347

hypothetical protein T03G11.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004
C;Accession: T29926
S;Gattung, S. attung, November 1995
A;Description: The sequence of C. elegans cosmid T03G11.
A;Reference number: Z20709
A;Reference number: Z20709
A;Accession: T29926
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-631 <GEI>A;CESP:T03G11.1
C;Genetics: C;Genetics: UNIPROT:Q22126; EMBL:U41272; PIDN:AAA82452.1; CESP:T03G11.1

Ajdene: CESP:T03G11.1 AjIntrone: 107/3; 214/3; 250/1; 306/2; 364/3; 405/2; 451/3; 522/1; 576/2

Gaps ö Query Match 79.5%; Score 35; DB 2; Length 631; Best Local Similarity 87.5%; Pred. No. 35; Matches 7; Conservative 1; Mismatches 0; Indels

ö

2 RLTKRGLK 9

à

N

DNA topoisomerase

Length 840;

```
Rightses, J.L.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A: Pescription: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A; Reference number: A82870
A; Accession: P82937
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-840 <cinA>
A; Residues: 1-840 <cinA>
A; Residues: 1-840 <cinA>
A; Coss-references: GB: AE002107; GB: AF222894; NID: g6899022; PIDN: AAF30487.1; GSPDB: GN0011
A; Experimental source: serovar 3; blovar 1
                                                                                                                                                                                                                                                                                                                     A;Gene: gyrA; UU082
A;Genetic code: SGC3
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4
                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                77.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 RLTKRGAK 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S66775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A35656
                                                                                                                                                                                                                                                                                                    C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                 procein B0205.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: A87912
C;Accession: A87912
C;Accession: A87912
C;Accession: A87912
C;Accession: A87912
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Retains preliminary
A;Molecule type: DNA
A;Residues: 1-99 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPROT: 061740; GB: chr_I; PIDN: AAC16987.1; PID: 93150469; GSPDB: GN000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77172
A;Accession: S77172
A;Accession: S77172
A;Retain: nucleic acid sequence not shown; translation not shown
A;Residues: 1-248 «KAN»
A;Residues: 1-248 «KAN»
A;Coss-references: UNIPROT:P73684; EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA1773
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A/Gene: gdh
C/Superfamily: ribitol dehydrogenase, short-chain alcohol dehydrogenase homology
F/6-186/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucose dehydrogenase - Synechocystis sp. (strain PCC 6803)
N/Alternate names: protein sll1709
C/Species: Synechocystis sp.
A/Variety: PCC 6803
C/Species: SAPAP-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S77172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 248; 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 2
Pred. No. 9.8;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.3%; Scor.
100.0%; Pred. No. 4...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 7; Conservative
||||:|||
539 RLTKQGLK 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 SKLTKRGVK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 RLTKRGL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLIKRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S77172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Cross-references:
C/Genetics:
A/Gene: B0205.5
A/Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
A; Molecule type: DNA
A; Residues: 1-2423 <ZUM>
A; Residues: 1-2423 <ZUM>
A; Residues: 1-2423 <ZUM>
A; Createrences: UNIPROT: P19158; UNIPROT: O13592; EMBL: Z74823; GSPDB: GN00015; MIPS: YOL
A; Experimental source: strain S288C
R; Alexandraki, D.; Katsoulou, C.; Tzermia, M.
B; Alexandraki, D.; Katsoulou, C.; Tzermia, M.
A; Reference number: S66756
A; Accession: S66774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: DNA
A.Residues: 1983-3079 «ALES-
A.Residues: 1983-3079 «ALES-
A.Farandau source: Errain S286C
A.Farandau, K.; Nakefuku, M.; Tamanoi, F.; Kaziro, Y.; Matsumoto, K.; Toh-e, A.
Mol. Cell. Biol. 10, 4303-4313, 1990
A.Title: IRA2, a second gene of Saccharomyces cerevisiae that encodes a protein with a d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-2308, 'V', 2310-2316, 'I', 2318-3079 <TAN>
A; Residues: 1-2308, 'V', 2310-2316, 'I', 2318-3079 <TAN>
A; Cross-references: EMBL: M33779; NID:g171761; PIDN: AAA34710.1; PID:g171762
B; Zumstein, E.; Griffin, H.; Schweizer, M.
Yeast 10, 1383-1387, 1994
A; Title: Sequence of a 10.27 kb segment on the left arm of chromosome XV from Saccharomy:
A; Reference number: S48253; MUID:95208358; PMID:7900427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-2423 <ZU2>
A;Cross.references: EMBL:X75449; NID:g414079; PIDN:CAA53202.1; PID:g414081
A;Ocross.references: EMBL:X75449; NID:g414079; PIDN:CAA53202.1; PID:g414081
A;Oce: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R;Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
Bubmitted to the EMBL Data Library, December 1994
A;Reference number: S50410
                                                                                                                                                                                                                                                                                                                                                                     probable GTPase-activating protein IRA2 - yeast (Saccharomyces cerevisiae)
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: $66774; $66774; Ā35656; $48254; $56426; $11190; $38505
$8.Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: $66775
        Gaps
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Accession: 548254
, Status: nucleic acid sequence not shown; translation not shown , Molecule type: DNA
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: S50426
A, Molecule type: DNA
A, Residues: 1-2423 <ZU3>
```

urealyticu

DNA topoisomerase chain A, DNA gyrase A subunit UU082 [imported] - Ureaplasma C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000

```
A; Molecule type: mRNA
A; Residues: 1-291 < PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A25267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A24684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A23817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A25266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A25774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A2967]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: 832802
R; Pape, M.B.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.B.; Marotti, K.R.; Melchic Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. Biochia. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 28-Dec-1887 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A26
C;Accession: A27850; I39474; I39469; I84624; I31179; PS0058
R;Ludwig; E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scd
A,71itle: DNA sequence of the human apolipoprotein B gene.
A;Reference number: A27850; MUID:88003974; PMID:3652907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: A27850
A,Molecule type: DNA
A,Molecule type: DNA
A,Rolecules: 1-617,'A', 619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,'
A,Crosd-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMNO; UNIF
R,Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A,Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A,Reference number: A91058; MUID:87161758; PMID:3030729
                                                                        AjGene: SGD:IRA2; MIPS:YOL081w
AjGene: SGD:IRA2; MIPS:YOL081w
AjGene: SGD:SO005441; MIPS:YOL081w
AjGene: SGD:SO005441; MIPS:YOL081w
AjGene: SGD:SO005441; MIPS:YOL081w
AjMap position: 151
CjSuperfamily: regulatory protein
F;Superfamily: ransmembrane #status predicted <TML>
F;1135-1151/Domain: transmembrane #status predicted <TML>
F;135-1151/Domain: transmembrane #status predicted <TML>
F;2318-2334/Domain: transmembrane #status predicted <TML>
F;2522-2578/Domain: transmembrane #status predicted <TML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Macaca fascicularis (crab-eating_macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
A; Cross-references: EMBL: X83121; NID: 9600461; PIDN: CAA58201.1; PID: 9600480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74 C;Species: Homo sapiens (man)
C;Species: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.3%; Score 34; DB 1; Length 3079; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA>
A;Note: 1109-Asp was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apolipoprotein B - crab-eating macaque (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.5; DE
Pred. No. 67;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apolipoprotein B-100 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.1%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRLTRKRGLK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3029 RLTKRGL 3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLT-KRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLTKRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: A25679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
Nucleic Acide Rees, 17, 19, 1911s, 5.C.; Pewell, L. M., Peese, R. J.; Insis, A. J.; Blackhart, B.; Noc. Nucleic Acide Rees, 17, 19, 1911s, 5.C.; Pewell, L. M., Peese, R. J.; Insis, A. J.; 19, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 1910s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s, 3131s,
```

```
A,Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                       A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su Freebeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. PEBS Lett. 170, 105-108, 1984 A.J. A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: Molecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleoside diphosphate kinase homolog ndk [imported] - Listeria monocytogenes (strain EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cipecies: Listeria monocytogenes (strain EC Cipecies: Listeria monocytogenes (strain EC Cipecies: Listeria monocytogenes (strain EC Cipace: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004  
Cipace: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004  
Cipaces D.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker. D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001  
Alauthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Marythler Comparative genomics of Listeria species.

A; Fitle: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <GLA>
A;Cross-references: UNIPROT:Q8Y5X4; GB:NC_003210; PIDN:CAD00007.1; PID:g16411382; GSPDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.1%; Score 33.5; DB 1; Length 4563; 90.0%; Pred. No. 4.5e+02; ive 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Nucleoside diphosphate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Experimental source: strain EGD-e C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3385 TRLTRKRGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A22006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
AI1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
A;Residues: 1671-2323,'PYW',2327-2352,'H',2354-2398 <hAR.>
A;Crose-references: GBMT/367; NID:9118731; PIDN:AAA51741.1; PID:9178732
R;Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.;
Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on A;Reference number: A90084; MUID:86130855; PMID:3841481
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Mesiduae: 3846-4298 (SHO>
R; Pfitzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seylar 367, 1077-1083, 1986
A; Title: Isolation, expression and characterization of a human apolipoprotein B 100-spec
A; Reference number: A25572; MUID:87076044; PMID:3024665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Molecule type: mRNA
A.Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39
A.Crose-references: GB.M12413; NID:9778735; PIDN:AAA51742,1; PID:9178736
R;Chen, S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cai
A;Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
A;Reference number: A40133; MUID:88018019; PMID:3659919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55
B; 1486-1499;1537-1556;1563-157;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-
A; Note: these fragments were derived from apo48
R; Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
B; Choman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
A; Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism F
A; Reference number: A28002; MUID:88106542; PMID:3426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricobs-Teleteures, us. N. 149uchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Blochem. Blophys. Res. Commun. 148, 279-288, 1987
A; Title: Identification of a novel in-frame translational stop codon in human intestine A; Reference number: A29659; MUID:88049670; PMID:2445342
A; Recession: A29659
A; Rocession: equence shown represents the carboxyl end of apolipoprotein B-48
A; Roces: the Sequence shown represents the carboxyl end of apolipoprotein B-48
C; Rim, T.W.; Meng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
Broc. Natl. Acad. Sci. US.A. 87, 5523-5527, 1990
A; Rite: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A; Contents: A35783; MUID:90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Readdues: 4219-4317, S;,4339-4563 <PFI>
A;Cross-references: GB:MA6676
R;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.
Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
A;Reference number: A24738; MUID:86042646; PMID:2932736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
./Residues: 3056-3159 <MEH>
./Gross-references: G8:X03045; NID:928783; PIDN:CAA26850.1; PID:9929609
./Hospattankar, A.V., Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
iochem. Biophys. Res. Commun. 148, 279-285, 1987
./Title: Identification of a novel in-frame translational stop codon in human intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: mRNA
A, Residues: 2129-2179, 2181-2235 < HA2>
A, Residues: 2129-2179, 2181-2235 < HA2>
A, Residues: 2129-2179, 2181-2235 < HA2>
A, Experimental source: intestine
A, NOte: this mRNA from intestine includes a stop codon created by RNA editing in place
B, Mehrabian, M. i, Schumaker, V.N.; Parsed, G.C.; West, R.; Johnson, D.F.; Kirchgessner, Nucleic Acids Res. 13, 6977-6953, 1985
A, Title: Human apolipoprotein B: identification of cDNA clones and characterization of a section of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the secon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: mRNA
A,Residues: 2165-2179 <CH1>
A,Residues: 2165-2179 <CH1>
A,Cross-references: GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:g178800
A,Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
A,Accession: A40133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A35783
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: A24269
```

1,

Gaps ä

DB 2; Length 147;

75.0%; Score 33;

Query Match

```
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell Rieger. M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon A, Authors. Schleich, S.; Schroeter, R.; Scoffone, F.; Seriguchi, J.; Sekowska, A.; Sero akcuchi, M.; Tamakoshi, A.; Tanaka, T.; Tengera, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Winters, M.; Vamane, K.; Yasumoto, K.; Yata, K.; Voshida, A.; Alathors: Voshikawa, H.; Zomantein, E.; Yoshikawa, H.; Danchin, A.
A.; Reference number: A69580; MUID: 98044033; PMID: 9384377
A.; Reference number: A69580; MUID: 98044033; PMID: 9384377
A.; Residues: 1-470 ckuv.
A.; Molecule type: DNA
A.; Residues: 1-470 ckuv.
A.; Residues: 1-470 ckuv.
A.; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Date: 23-Apr-1999 #sequence Database, Apr-1998
B;Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S51368
R;Turmel, M; Otis, C.
Curr. Genet. 27, 5416, 1994
A;Title: The chloroplast gene cluster containing psbF, psbL, petG and rps3 is conserved A;Reference number: S51365; MUID:95269309; PMID:7750147
A;Accession: S51368
A;Accession: S51368
A;Residues: 1-800 <TUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species; chloroplast Chlamydomonas eugametos
C;Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: 851368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: P46307; EMBL: L29282; NID: 9575472; PID: 9575476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: arginine permease
C;Keywords: amino acid transport; glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T05005
A;Molecule type: DNA
A;Residues: 1-633 <BBV>
A;Cross-references: UNIPROT:065655; EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19P19
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosomal protein S3 - Chlamydomonas eugametos chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T19P19.70 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 2
Pred. No. 68;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 2
Pred. No. 90;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4
A;Introns: 385/1; 448/1; 498/3
A;Note: T19P19.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.(
Best Local Similarity 87.!
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 TRLTKKGV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 RLTTRGLK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTKRGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Genome: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: rocc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: rps3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
S51368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Althernate names: protein ipa-77d
Cispecias: Bacillus subtilis
NiAlternate names: protein ipa-77d
Cispecias: Bacillus subtilis
Cipate: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
Cispecias: Bacillus subtilis
Cipate: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
CiAccession: S39733; G69693
Riclaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.D.; Gonzales, W.; Hullo, M.F.; Ionescu, A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
A.Title Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr A; Reference number: S39655; MUD:95020537; PMID:7934828
A.Accession: S39733
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: S39655; MUD:95020537; PMID:7934828
A.Reference number: No.; Moszer, I.; Albertini, A.M.; Alloni, G.; Rarer, N.M.; Chq.
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Rabret, C.; Ferrari, B.
A.Ruthors: Foulger, D.; Fritz, C.; Fujitz, M.; Rutita, Y.; Fuma, S.; Galler, A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: 332687
A,Mccession: 332687
A,Mccession: 332687
A,Rocession: 332687
A,Mccession: Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By Size By S
                                                                                                                                                                                                                                                                                                                                                                                              ribosomal protein S13.e, cytosolic - nematode (Brugia pahangi)
N'Alternate names: 17.4K protein
C;Species: Brugia pahangi
C;Species: Brugia pahangi
C;Date: 30-Sep-1991 #sequence revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S32687; S14440; $06771
C;Accession: S12687; S14440; $06771
Submitted to the EMBL Data Library, January 1992
A;Description: Developmental modulation of relative gene numbers in a parasitic nematode
                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indela
                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1;
Pred. No. 23;
2; Mismatches 1
            d. No. 23;
Mismatches
                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%;
        66.7%;
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                      ||: |:|||
TRIEKKGLK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| |:||:
TRLAKKGLR 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTKRGLK 9
                                                                                                                              1 TRLTKRGLK
            Best Local Similarity
                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38
                                            Matches
                                                                                                                              ઠે
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
```

```
129 QLTKRGVK 136
                                                                        :||||||
61 ITKRGLK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 RLTKRGLK 9
                                     3 LTKRGLK 9
                                  à
                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: mRNA
A;Residues: 1-114 <MUE>
A;Residues: 1-114 <MUE>
A;Residues: 1-114 <MUE>
A;Residues: 1-114 <MUE>
A;Residues: 1-114 <MUE>
B;Cross-references: UNTROT:P47922; EMBL:X86474; NID:g895846; PIDN:CAA60198.1; PID:g8958
B;Kennedy, J; Kelner, G.S.; Kleyensteuber, S.; Schall, T.J.; Weiss, M.C.; Yssel, H.; Sc
J: Immunol. 155, 203-209, 1995
A;Title: Molecular cloning and functional characterization of human lymphotactin.
A;Reference number: 138978; MUID:95325590; PMID:7602097
                                                                                                                                                                                                                                                                                                                                                                                  Jymphotactin precursor - human
N.Alternate names: activation-induced chemokine-related protein (ATAC); single cysteine
N.Alternates: eosinophilotactic peptide
C.Species: Homo sapiens (man)
C.Date: 23-Oct-1981 #sequence revision 07-Jun-1996 #text_change 09-Jul-2004
C.Accession: 860650; 189878; A03180; 153506
R.Mueller, S.; Dorner, B.; Korthaeuer, U.; Mages, H.W.; D'Apuzzo, M.; Senger, G.; Krocze
A.Title: Cloning of ATAC, an activation-induced, chemokine-related molecule exclusively
A.Reference number: 860650; MUID:95339892; PMID:7615002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Residues: 1-114 <KEN>
A.Cross-references: EMBL:U23772; NID:g902001; PIDN:AAC50164.1; PID:g902002
R.Goetal, E.J.; Austen, K.F.
Proc. Natl. Acad. Sci. U.S.A. 72, 4123-4127, 1975
A.Title: Purification and synthesis of ecsinophilotactic tetrapeptides of human lung tis A.Reference number: A03190; MUID:76078412; PMID:1060093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Cross-references: GB:143768; NID:9927650; PIDN:BAA07825.1; PID:9927651
C;Comment: Lymphotactin is produced by activated T-cells and is chemotactic for some lym C;Comment: Eosinophilotactic peptide is released from mast cells in lung and other tissu ially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of en C;Comment: It has not yet been shown that the previously detected eosinophilotactic pept
                                                                                                                                             ö
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Keywords: Chemotaxis; cytckine; lymphokine; mast cell; T-cell 18.115/Domain: signal sequence #status predicted <81G>.15/Domain: propeptide #status predicted <PRO>. F;22-114/Product: propeptide #status predicted <PRO>. F;22-114/Product: lymphotactin #status predicted <MAT>. F;22-25/Product: eosinophilotactic peptide #status predicted <BOP>. F;32-69/Disulfide bonds: #status predicted
                                                              75.0%; Score 33; DB 2; Length 800; 77.8%; Pred. No. 1.16+02; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 114;
C;Keywords: chloroplast; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB
Pred. No. 29;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: 138978
A, Status: translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-114 <YOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: GDB:SCYC1; LTN; LPTN; ATAC A;Cross-references: GDB:682094 A;Cross-references: GDB:682095 C;Superfamily: Lymphotactin C;Keywords: chemotaxis; cytokine; lym F;Lef/Domain: signal sequence #statur F;6-21/Pomain: prope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 85.7%; 6; Conservative 1
                                                                                                                                                                                                                                        266 TKLTKROLK 274
                                                                                                                                                                               1 TRLTKRGLK 9
                                  Query Match
Best Local Similarity
....hes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                               ò
                                                                                                                                                                                                                                        셤
```

ö

Gaps

ö

0; Indels

```
Fightime S. Y.; Neuhard, J. 1994
J. Bacteriol. 176, 3698-3707, 1994
A; Eference number: 140166; MUID:94266723; PMID:8206848
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-257 < RES.
                                                                                                                                                                                                                                                                                    A, Cross references: UNIPROT: P46536; EMBL: X73308; NID: 9312439; PIDN: CAA51740.1; PID: 93124
C; Superfamily: cytochrome-c3 hydrogenase gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
hypothetical protein 2 - Bacillus caldolyticus
CiSpecies: Bacillus caldolyticus
CiSpecies: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                          Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 2;
Pred. No. 62;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: December 29, 2004, 12:39:10 Job time : 10.6932 sece
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                    C; Accession: I40170; S34322
```

Н

```
Arthrobacter ilicis.
                                                                                                                                                                                                                                                                                                                           423 AA;
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=43665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPA (Fragment)
                                                                                                                                                      Q7WSQ9;
01-OCT-2003 (
01-OCT-2003 (
Name=PPA
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Q8QH16,
Q8QH16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus
                                                                                                                                                Q7WSQ9
                                                                                                                                  RESULT 1
Q7WSQ9
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                 DBOHI6
                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                        Q75tn6 bacillus in Q75tn6 bacillus al Q75tx1 bacillus ha Q75tx3 bacillus ha Q75tx5 bacillus ha Q75tx7 bacillus ha Q75tx8 bacillus ha Q75tx8 bacillus ha Q75tx8 bacillus ha Badi8155 bacillus Badi8156 bacillus Badi8156 bacillus Badi8156 bacillus
                                                                                                                                                                                                                                                                                                       Q8qhi6 gallus gall
Q8bid8 mus musculu
Q8nle6 homo sapien
Q75tw9 bacillus ha
Bad18188 bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                   bacillus
bacillus
bacillus
                                                                                                                                                                                                                                                                                                27wsq9 arthrobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bacillus
                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                             December 29, 2004, 12:13:11 ; Search time 52.5682 Seconds (without alignments) 98.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bad18159 h
Bad18160 h
Bad18161 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bad18162 Bad18180 Bad18181 Bad18181 Bad18183 Bad18183 Bad18183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bad18185 b
Bad18186 b
Bad18256 b
Bad18259 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bad18184
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                          1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                       Q8QHI6
FXLE_MOUSE
FXLE_HUMAN
Q75TW9
BAD18188
                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                           BAD18160
BAD18161
BAD18162
BAD18180
BAD18181
BAD18183
BAD18184
BAD18185
BAD18186
BAD18259
                                                                                                                                                                                                                                                                                                                                                                                                                      BAD18157
BAD18158
                                                                                                                                                                                                                                                                                                                                                                                                                 BAD18156
                                                                                                                                                                                                                                                                                                                                                                                                                                     BAD18159
                                                                                                                                                                                                                                                                                                                                                  Q75TQ1
Q75TX1
Q75TX3
Q75TX6
Q75TX7
Q75TZ5
Q75TZ5
                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                          075TN6
                                                                                                                                                                                                                                                                                                                                                                                                        Q9K5P7
                                                                                                                                                                                                      UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                           Post-processing: Minimum Match 0%
                                                                          US-09-823-418-14
                                                                                                                                                                                                                                                                                   B
                                                                                        TRLTKRGLK 9
                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                        Sequence:
                                                                                                                           Searched:
                                                                                                                                                                                                       Database
                                               Run on:
                                                                                                                                                                                                                                                                            Result
No.
```

```
32 36 81.8 427 2 BAD18271 Bad18271 bacillus Q6cld8 kluyveromyc G0cld8 kluyveromyc G0cld8 kluyveromyc G0cld8 kluyveromyc G0cld8 kluyveromyc G0cld8 kluyveromyc G0cld8 kluyveromyc G0cld8 kluyveromyc G0cld9 kluyveromyc G0cld7 G0cld8 kluyveromyc G0cld7 G0cld8 kluyveromyc G0cld7 G0cld9 kluyveromyc G0cld7 G0cld9 kluyveromyc G0cld9 kluyveromyc G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9 G0cld9
```

# ALIGNMENTS

```
PARAIN-Rucela,
MEDLINE-22753791; PubMed=12730200;
MEDLINE-22753791; PubMed=12730200;
Parschat K., Hauer B., Kappl R., Kraft R., Huettermann J., Fetzner S.;
Parschat K., Hauer B., Kappl R., Kraft R., Huettermann J., Fetzner S.;
"Gene Cluster of Arthrobacter ilicis R.61a Involved in the Degradation of Quinaldine to Anthranilate. Characterization and Functional
Expression of the Quinaldine 4-oxidase qoxLMS Genes.";
J. Biol. Chem. 278:27483-27494 (2003).
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; P:transporter activity; IEA.
GO; GO:0006810; P:transporter activity; IEA.
InterPro; IPR00714; MFS.
PROSITE; PS50850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43696 MW; BB11CBADA85DF241 CRC64;
                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2;
Pred. No. 8.3;
1; Mismatches
                                                                                                                                                                                                                       Micrococcineae; Micrococcaceae; Arthrobacter.
423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
PRT;
                                                                                                                                       Putative transporter protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86...
Best Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 TRLTKOGLK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TRLTKRGLK 9
```

ö

~

```
1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESENDENCE FROW N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

RESPONDENCE FROM N.A.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRILE MOUSE STANDARD; PRT; 400 AA.
QBBIDB; QBR5H7; QBVDT7; Q922N5;
QBSIDB COUG. (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last agenence update)
05-JUL-2004 (Rel. 44, Last annotation update)
F.box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
MEDLINE=21972450; PubMed=11976951;
Das T., Purkayastha-Mukherjee C., D'Angelo J., Weir M.;
"A conserved F-box gene with unusual transcript localization.";
Dev. Genes Evol. 212:134-140(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                                                                                                                                                                                                                                                                                                                                                                              86.4%; Score 38; DB 2; Length 188; 77.8%; Pred. No. 9.6; tive 2; Mismatches 0; Indels
                                                                                                                                                  Das T.K., Purkayastha-Mukherjee C., D'Angelo J., Weir M.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; A4467464; AALT5968.1; -. InterPro; IPR001611; LRR. InterPro; IPR001611; LRR. PFam; PF00560; LRR; 4.
                                                                                                                                                                                                                                                                                                                                   188 188
188 Aa; 20629 MW; 21702832DA5CE865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 77.8%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Fbx114; Synonyms=Ppa;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 420:563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 TRITKRGLE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTKRGLK 9
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                             TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
  HERET REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REARES REA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
```

```
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Machaner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altaoner R.D., Colline F.S., Wagger L., Schaefer C.R., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Develor B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
A stapleton M., Soares M.B., Parmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schent J.E., Jones S.J.M., Marra M.A.;
R. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 22 V -> F (in Ref. 2; AAH21329).
400 AA; 43864 MW; E0B297E4B4F83C22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.4%; Score 38; DB 1;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AK084506, BAC39201.1; --
EMBL, BC006913, AAH06913.1; --
EMBL, BC021329, AAH21339.1; --
EMBL, AF467463, AAL75967.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001810; F-box.
InterPro; IPR001611; IRR.
InterPro; IPR007089; IRR cys.
InterPro; IPR008945; Skpl_Skp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leucine-rich repeat; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:2141676; Fbx114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00646; F-box;
Pfam; PF00560; LRR; 6.
```

m

```
418 AA; 45886 MW; 5779961C8177779F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAD18188;
BAD18188;
01-JUN-2004
01-JUN-2004
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH9065301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                Q75TW9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
BAD18188
                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                      HID DE REPRESENTATION OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSGERFFE
                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Lung;

X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Fedigodd B.A., Grouse L.H., Derge J.G.,

RA Altaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.P., Ordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farner G.M., Rubin G.M., Hong L.,

A Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Wordin T.B., Sodergren R.D., Mullahy S.J.,

Raha S.S., McZwan P.J., McKerman K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Gren E.D., Dickson M.C.,

RA Schnertield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Schnertion and initial analysis of more than 15,000 full-length human

RT and mouse CDNA sequences ";

Procteins and promotes their ubiquitination and degradation.

C. -- FUNCTION: Probably recognizes and binds to some phosphorylated

C. -- SUBUNIT: Part of a SCF (SKPI-cullin-F-box) protein ligase complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the complex for the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                         05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last amotation update)
P-box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).
--- SIMILARITY: Contains 1 F-box domain.
--- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leucine-rich repeat; Repeat; Übl conjugation pathway.

REPEAT 20 120 LRR 1.

REPEAT 203 231 LRR 2.

REPEAT 203 231 LRR 3.

REPEAT 254 280 LRR 4.

REPEAT 331 356 LRR 6.
                                                                                                                                          418 AA.
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC028132; AAH28132.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001810; F-box.
InterPro; IPR001611; LRR.
InterPro; IPR007089; LRR_Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:28624; FBXL14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00646; F-box; 1.
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00560; LRR; 6.
367 TRITKRGLE 375
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                      Name=FBXL14;
                                                                                                                                    FXLE HUMAN
                                                                                                         PXLE HUMAN
셤
```

```
ö
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takami H., Han C., Takaki Y., Ohtsubo E.; "Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125."; J. Bacteriol. 183:4345-4356(2001).
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AH-101;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui Takami H., Nakasone K., Takaki Y., Ogasawara N., Kuhara S., Horikoshi K.;
                 Score 38; DB 1; Length 418;
Pred. No. 22;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 36; DB 2; Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takani H., Matsuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126496; BAD1081891;
InterPro; IPR00346; Transposase 20.
InterPro; IPR00355; Transposase 20.
Ffam; PF0271; Transposase 20.
Pfam; PF0271; Transposase 20.
Pfam; PF01848; Transposase 9; 1.
SEQUENCE 423 AA; 48264 WW; 72B7EDDE480E9BAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                       OS-JUL-2004 (TERMELrel. 27, Ca
05-JUL-2004 (TERMELrel. 27, La
05-JUL-2004 (TERMELrel. 27, La
Transposase of 18653.
                        86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 27, (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.8%;
Query Match
Best Local Similarity 77.0
77.0
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                      Q75TW9;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                367 TRITKRGLE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 rkirkkick 347
                                                                                                        1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2004 (TrEMBLre
Transposase of IS653
                                                                                                                                                                                                                                                                                                                                                                               ORFNames=BH9065301;
Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=AH-101;
PubMed=11418576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AH-101;
```

ô

Gapa

ö

Indels

```
"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=11418576,
Takani H., Han C., Takaki Y., Ohtsubo E.;
Tidentification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAINDSM485,
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                            81.8%; Score 36; DB 2; Length 427; 77.8%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEWBLrel. 27, Created)
05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEWBLrel. 27, Last annotation update)
05-JUL-2004 (TrEWBLrel. 27, Last annotation update)
Transposase of IS650 (Transposase of IS653).
0RFNames=BAL065001, BAL065301,
Bacillus alcalophilus
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                (NOV-2003) to the EMBL/GenBank/DDBJ databases
                      Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases EMBL; AB126567; BAD18271.1; ...
InterPro; IPR003346; Transposase 20.
InterPro; IPR002525; Transposase 9.
Pfam; PP0271; Transposase 20; 1.
Pfam; PF01548; Transposase 20; 1.
Pfam; PF01548; Transposase 9; 1.
SEQUENCE 427 AA; 48654 MW; B812714B694F3C88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takami H., Matsuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126554; BAD18256.1; -.
EMBL; AB126557; BAD18259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 AA; 48754 MW; B3B77D309F000033 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.8%; Score 36; DB 2;
77.8%; Pred. No. 60;
ive 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 AA
                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003346; Transposase_20.
InterPro; IPR002525; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
Pfam; PF01548; Transposase_9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.0
77 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 rkirkkicki 347
                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLIKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=DSM485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DSM485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q75TQ1,
Q75TQ1,
05-JUL-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q75TX1
Q75TX1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
Q75TX1
ID Q75TX
                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOSOR OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                    Takami H., Han C., Takaki Y., Ohtsubo E., Indentification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.", J. Bacteriol. 183:4345-4356 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM12;
PubMed=11418576;
Pakami H., Han C., Takaki Y., Ohtsubo E.;
Tidennification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                                                                                    Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AH-101,
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Wide-range distribution of insertion sequences identified in B. halodurans among bacilli and a new transposeon disseminated in alkaliphilic and thermophilic bacilli.";
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126496; BAD18188.1;
SEQUENCE 423 AA; 48264 MW; 72B7EDDE480E9BAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DSM12;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
Fakami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           °
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 36; DB 2; Length 423; 77.8%; Pred. No. 60; 1; Indels rative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 AA
                                                                                                                                                                                                                                                                                                                                          STRAIN=AH-101;
MEDLINE=20512582; PubMed=11058132;
Tabaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-DSM12;
Takami H., Matsuki A., Takaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transposase of 18653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORFNames=BFI065301;
Bacillus firmus.
                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
         NCBI_TaxID=86665;
                                                                                             STRAIN=AH-101;
PubMed=11418576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q75TN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCOS SERVICE REPORTS TO SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

Gaps

ö

1; Indels

Length 427;

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
Takami H., Han C., Takaki Y., Ohtsubo E.; "Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125."; J. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami H., Han C., Takaki Y., Ohtsubo E.; Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125."; Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20512582; PubMed=11058132;
Takani H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Puji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.8%; Score 36; DB 2; Length 427; 77.8%; Pred. No. 60; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=86665;
                                                                                                                                                                                          STRAIN-DSM6940;
Takami H., Matsuki A., Takaki Y.;
Submitted (NOV-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126492; BAD16184.1; -.
InterPro; IPR003346; Transposase_20.
InterPro; IPR003525; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
SEQUENCE 427 AA; 48726 WW; ED574C089EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takami H., Matsuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB126489; BAD18181.1;
InterPro; IPR00346; Transposase 20.
InterPro; IPR00355; Transposase 20.
Pfam; PF0271; Transposase 20.
Pfam; PF0271; Transposase 20.
Pfam; PF01548; Transposase 20.
SEQUENCE 427 AA; 49016 WW; D89A03BD5B14AE81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 81.8%; Score 36; DB 2; Best Local Similarity 77.8%; Pred. No. 60; Matches 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fransposase of IS653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=BH2065301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11418576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q75TX6
Q75TX6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
             REAL REAL BOOK SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO OR SELVEN SO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takami H., Han C., Takaki Y., Ohtsubo E.; "Identification and distribution of new insertion sequences in the "Indentification and distribution of alwaliphilic Bacillus halodurans C-125."; U. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                      MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DSM6940;
MEDLINE-20512582; PubMed=11058132;
Madami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.8%; Score 36; DB 2; Length 427; 77.8%; Pred. No. 60; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DSM9774;
Takami H., Matenki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126494; BAD18186.1; -.
                                                                                                                                                                                   Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001346; Transposase_20.
InterPro; IPR002525; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
SEQUENCE 1548; Transposase_9; 1.
SEQUENCE 427 AA; 48724 WW; 332EABOF1B1815A0 CRC64;
      05-JUL-2004 (TrEMBLrel. 27, Created)
5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transposase of IS653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transposase of IS653.
ORFNames=BH5065301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTKRGLK 9
                                                                                                                                                            Bacillus halodurans
                                                                                                                                  ORFNames=BH7065301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus halodurans
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=DSM9774;
PubMed=11418576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DSM6940;
PubMed=11418576;
                                                                                                                                                                                                                                                                                                                            STRAIN=DSM9774;
```

Query Match

8 셤 Q75TX3

RESULT 10

ö

```
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               STRAIN=C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q75TZ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=DSM497;
PubMed=11418576;
Takami H., Han C., Takaki Y., Ohtsubo E.;
"Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                                            STRAIN-DSM497;
BELINRE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20512582; PubMed=11058132;
Takami H., NakaBone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 81.8%; Score 36; DB 2; Length 427; Local Similarity 77.8%; Pred. No. 60; length 427; les 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DSM497;
Takani H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126488; BAD10180-1;
EMBL; AB126464; BAD18156-1;
                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, NCBI TaxID=86665,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B3B77D309F000033 CRC64;
                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
17ansposase of IS653 (Transposase of IS650)
08-Names=BH1065001, BH1065301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                              427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003346; Transposase 20.
InterPro; IPR002525; Transposase 9.
Pfam; PF0217; Transposase 20; 1.
SEQUENCE 427 AA; 48754 WW; B3B77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Cr
05-JUL-2004 (TrEMBLrel. 27, La
05-JUL-2004 (TrEMBLrel. 27, La
Transposase of IS650.
ORFNamee=EH806501;
Bacillus halodurans.
                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes,
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                     Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                     Q75TX7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q75TZ5
                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Locy
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                   075TX7
                                                                                                                           ACCOS ON THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION 
셤
```

ò g 

```
"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtills."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of the alkaliphillc bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                             PubMed=11418576, Takaki Y., Ohtsubo E.; Takami H., Han C., Takaki Y., Ohtsubo E.; Takami H., Han C., Takaki Y., Ohtsubo E.; Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125."; J. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=DSM8718, DSM9774, and DSM6939;
STRAIN=DSM8718, DSM9774, and DSM6939;
BubMed=11418576;
Takami H., Han C., Takaki Y., Ohtsubo E.;
"Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DSM8718, DSM9774, and DSM6939;
STRAIN-DSM8718, DSM9774, and DSM6939;
MDLINES-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
1Tansposase of IS650 (Transposase of IS653).
ORFNames=BH4065001, BH4065301, BH6065001, BH6065301, BH7065001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Takami H., Matsuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AB126470; BAD18162.1; -
InterPro; IPR003346; Transposase 20.
InterPro; IPR003525; Transposase—9.
Pfam; PP02371; Transposase—9.
Pfam; PP02371; Transposase—9.
Pfam; PP02486; Transposase—9; 1.
SEQUENCE 427 AA; 48726 MW; 14692A5DC572A2B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DSMB718, DSM9774, and DSM6939;
Takami H., Mateuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126469; BAD18160.1;
EMBL; AB126469; BAD18161.1;
EMBL; AB126491; BAD18183.1;
EMBL; AB126491; BAD18185.1;
EMBL; AB126466; BAD18185.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, NCBI_TaxID=86665,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 2;
Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.8%;
```

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami H., Han C., Takaki Y., Ohtsubo E.;
Takami H., Han C., Takaki Y., Ohtsubo E.;
Takami H., Han C., Takaki Y., Ohtsubo E.;
Takami H., Han C., Takaki Y., Ohtsubo E.;
Tafentification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).

B. Bacteriol. 183:4345-4356(2001).

C. TRAIN-DSM6940;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Takami H., Tanasposase_20.

R. InterPro; IPR001346; Transposase_20.

R. InterPro; IPR002525; Transposase_20.

R. Pfam; PF01371; Transposase_20; 1.

R. Pfam; PF01548; Transposase_20; 1.

R. Pfam; PF01548; Transposase_20; 1.

R. Pfam; PF01548; Transposase_20; 1.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=DSM6940;
MBDLINE=20512582;
MBDLINE=20512582;
Puji N., Nakagone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                            Query Match 81.8%; Score 36; DB 2; Length 427; Best Local Similarity 77.8%; Pred. No. 60; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 81.8%; Score 36; DB 2; Length 427; Best Local Similarity 77.8%; Pred. No. 60; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transposase of 18650.

ORFNames=BH5065001;

Bacilius halodurans.

Bacilius halodurans.

NCBI_TaxID=86665;
InterPro; IPR003346; Transposase_20.
InterPro; IPR002525; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
Pfam; PF01548; Transposase_9; 1.
SEQUENCE 427 AA; 48696 WW; F14A8D5B2B009CB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 TRITKRGRK 347
                                                                                                                                                                                                                                                                                                                                                                       1 TRLIKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTKRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=DSM6940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            075TZ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
OCYST28
AC OCYST28
AC OCYST28
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-JUJ
DT OS-
                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

Search completed: December 29, 2004, 12:37:39 Job time : 53.6793 secs

INS PORCE OF THE PROPERTY OF T